

4 protein - protein search, using sw model					
April 19, 2001, 12:56:42 ; Search time 22.16 Seconds (without alignments)					
582.982 Million cell updates/sec					
title: US-09-441-723-1					
target score: 226					
sequence: 1 MGPLPRTVELFYDVLSSYSW.....AHLLGEKWMGPIPPAVNARL 226					
scoring table: OLIGO Gapop 60.0 , Gapext 60.0					
searched: 390729 seqs, 57163235 residues					
word size : 0					
total number of hits satisfying chosen parameters:					
minimum DB seq length: 0					
maximum DB seq length: 2000000000					
post-processing: Listing first 45 summaries					
database :					
A_Geneseq_0401.*					
1: /SIDSL1/gcgdata/geneseq/geneseqp/AA1980.DAT:*					
2: /SIDSL1/gcgdata/geneseq/geneseqp/AA1981.DAT:*					
3: /SIDSL1/gcgdata/geneseq/geneseqp/AA1982.DAT:*					
4: /SIDSL1/gcgdata/geneseq/geneseqp/AA1983.DAT:*					
5: /SIDSL1/gcgdata/geneseq/geneseqp/AA1984.DAT:*					
6: /SIDSL1/gcgdata/geneseq/geneseqp/AA1985.DAT:*					
7: /SIDSL1/gcgdata/geneseq/geneseqp/AA1986.DAT:*					
8: /SIDSL1/gcgdata/geneseq/geneseqp/AA1987.DAT:*					
9: /SIDSL1/gcgdata/geneseq/geneseqp/AA1988.DAT:*					
10: /SIDSL1/gcgdata/geneseq/geneseqp/AA1989.DAT:*					
11: /SIDSL1/gcgdata/geneseq/geneseqp/AA1990.DAT:*					
12: /SIDSL1/gcgdata/geneseq/geneseqp/AA1991.DAT:*					
13: /SIDSL1/gcgdata/geneseq/geneseqp/AA1992.DAT:*					
14: /SIDSL1/gcgdata/geneseq/geneseqp/AA1993.DAT:*					
15: /SIDSL1/gcgdata/geneseq/geneseqp/AA1994.DAT:*					
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18: /SIDSL1/gcgdata/geneseq/geneseqp/AA1997.DAT:*					
19: /SIDSL1/gcgdata/geneseq/geneseqp/AA1998.DAT:*					
20: /SIDSL1/gcgdata/geneseq/geneseqp/AA1999.DAT:*					
21: /SIDSL1/gcgdata/geneseq/geneseqp/AA2000.DAT:*					
22: /SIDSL1/gcgdata/geneseq/geneseqp/AA2001.DAT:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
No.	Score	Query Match Length	DB ID	Description	
1	226	100.0	226	21	Novel human glutathione S-transferase, GSTS.
2	226	100.0	256	20	Human endometrium
3	131	58.0	131	21	Human secreted protein
4	97	42.9	97	21	Human secreted protein
5	88	38.9	300	21	Human secreted protein
6	12	5.3	97	21	Gene 45 human secreted protein
7	8	3.5	179	21	Lung cancer associated protein
8	8	3.5	195	21	Human M2 protein
9	8	3.5	283	21	Human M4 protein
10	8	3.5	813	19	Salmonella enteritidis
					Sequence: 1922572.
RESULT					
1	Y77499	standard; Protein: 226 AA.			
ID	Y77499	ID Y77499 standard; Protein: 226 AA.			
XX	XX	XX			
AC	AC	AC Y77499;			
XX	XX	XX			
DT	DT	05-JUN-2000 (first entry)			
DE	DE	Novel human glutathione S-transferase, GSTS.			
XX	XX	XX			
KW	KW	Glutathione S-transferase; human; GSTS; cancer; immune disorder; gene therapy; diagnosis; treatment; drug screening.			
XX	XX	XX			
OS	OS	Homo sapiens.			
XX	XX	XX			
PR	PR	PR 25-NOV-1997; 97US-0978174.			
XX	XX	XX			
PA	PA	(INCYT) INCYTE PHARM INC.			
PI	PI	Hillman JL, Shah P, Lal P, Corley NC;			
DR	DR	DR WPI: 2000-205304/18.			
N-PSDB	N-PSDB	N-PSDB; Z02593.			
Isolated nucleic acid encoding glutathione S-transferase useful in the production of agents for preventing, diagnosing and treating diseases associated with cell proliferation -					

PS Claim 8; Fig 1A-C; 27pp; English.

XX This sequence represents a novel human glutathione S-transferase, GSTS.

CC Nucleotide sequences encoding GSTS were initially isolated from a urologic cDNA library, and subsequently extended using cDNA libraries derived from other tissues, such as brain or bladder. The present sequence is encoded by a consensus cDNA. GSTS, and nucleotides which encode it may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GSTS expression, such as cancers and immune disorders. Nucleotides which encode GSTS may be used in gene therapy to treat disorders associated with reduced expression or activity of GSTS, and in antisense therapy for disorders associated with increased GSTS expression or activity. They may also be used for the recombinant production of GSTS, and as a source of probes and primers to detect and quantitate the presence of similar nucleic acid sequences, particularly for the diagnosis of GSTS-associated disorders. GSTS proteins may be used as antigens in the production of antibodies against GSTS and in assays to identify modulators (agonists and antagonists) of GSTS expression and activity. The anti-GSTS antibodies and GSTS antagonists may also be used to downregulate GSTS expression and activity. Antagonists of GSTS expression and function may be used to treat immune disorders (e.g., AIDS, anaemia, asthma, Crohn's disease, irritable bowel syndrome, multiple sclerosis, osteoarthritis, microbial infections) and cancers (e.g., leukaemia, lymphoma, melanoma, and cancers of the breast, prostate, liver, lung and brain). The anti-GSTS antibodies may also be used as diagnostic agents.

XX Sequence 226 AA;

Query Match 100.0%; Score 226; DB 21; Length 226;

Best Local Similarity 100.0%; Pred. No. 2.5e-219; Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPLPRTVELFDVLSPLSPYSPWLGPFETLCRYQNTWNINQLRPLSLITGIMKDSGNKPPGLLP 60

Db 1 mgp-prtvelfdvlsplspwy...feilcrgnwniinqrls...itqimkdsqnkppgl... 60

Qy 61 RKGLYMANDLKLRRHLQLQIPTHPKFLSYMLFEKGSLSAMRFLTAVNLEHPEMLEKASRE 120

Db 61 rkglymandlklrrhlqlqipthpkflsymlfe...ekgs...samrfltavnl...epmleka... 120

Qy 121 LWMRWWSRNEDITEPOSTIILAAEAKAGMSAEQAGLLEKIAATPKVKNQKETTEAACRYGA 180

Db 121 lwmrw...rnedite...g...aaeakagmsaeqagg...ekiaatpkvk...q...ketteaacryga 180

Qy 181 FGLPITVAHDGQTHMLFGSDRMELLAHLIGEKWMGTIPPAYNARL 226

Db 181 fglpitva...hdg...qthmlf...sdrmel...lligekwm...gtippaynarl 226

RESULT 2 Y59988 standard; Protein: 256 AA.

AC Y59988;

XX 31-JAN-2000 (first entry)

XX Human endometrium tumour EST encoded protein 48.

XX Endometrium; human; tumour; cancer; anticancer; cytostatic; EST:

XX treatment; uterine; gene therapy; expressed sequence tag.

OS Homo sapiens.

XX DE19811948-A1.

XX PN EP1033401-A2.

XX PR 17-APR-1998; 98DE-1017948.

XX PR 17-APR-1998; 98DE-1017948.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX DR WPI: 1999-591957/51.
 XX DR N-FSDB; Z41996.
 XX PR New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial cancer
 PT and identification of therapeutic agents -
 XX PS Claim 23; Page 294; 444PB; German.
 XX
 CC This invention describes novel human nucleic acid (cDNA) sequences (A),
 CC that are highly expressed in uterine tumour tissue and which have
 CC anticancer and cytostatic activity. (A) are used (i) for recombinant
 CC expression of polypeptides (B) and (ii) to isolate complete genes. (B)
 CC are used (i) to identify agents suitable for treatment of uterine or
 CC endometrial cancer; (ii) directly for treating these forms of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of the
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. Y59911-y60328 represent protein
 CC fragments encoded by the human endometrium tumour cDNA library derived
 CC EST fragments represented in Z41981-242121.
 XX SQ Sequence 256 AA:
 Query Match 100.0%; Score 226; DB 20; Length 256;
 Best Local Similarity 100.0%; Pred. No. 2.8e-219;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGPLPRTVELFDVLSPLSPYSPWLGPFETLCRYQNTWNINQLRPLSLITGIMKDSGNKPPGLLP 60
 Db 31 mgplprtvelfdvlsplspwy...feilcrgnwniinqrls...itqimkdsqnkppgl... 60
 Qy 61 RKGLYMANDLKLRRHLQLQIPTHPKFLSYMLFEKGSLSAMRFLTAVNLEHPEMLEKASRE 120
 Db 91 rkglymandlklrrhlqlqipthpkflsymlfe...ekgs...samrfltavnl...epmleka... 120
 Qy 61 RKGLYMANDLKLRRHLQLQIPTHPKFLSYMLFEKGSLSAMRFLTAVNLEHPEMLEKASRE 120
 Db 91 rkglymandlklrrhlqlqipthpkflsymlfe...ekgs...samrfltavnl...epmleka... 150
 Qy 121 LWMRWWSRNEDITEPOSTIILAAEAKAGMSAEQAGLLEKIAATPKVKNQKETTEAACRYGA 180
 Db 151 lwmrw...rnedite...g...aaeakagmsaeqagg...ekiaatpkvk...q...ketteaacryga 210
 Qy 181 FGLPITVAHDGQTHMLFGSDRMELLAHLIGEKWMGTIPPAYNARL 226
 Db 211 fglpitva...hdg...qthmlf...sdrmel...lligekwm...gtippaynarl 226
 RESULT 3 G01523
 ID G01523 standard; Protein: 131 AA.
 AC G01523;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein, SEQ ID NO: 5604.
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX PR 06-SEP-2000.

XX	28-SEE-2000.
PF	21-FEB-2000; 2000EP-0200610.
PF	16-MAR-2000; 2000WO-US06824.
XX	PR 26-FEB-1999; 99US-0122487.
PR	19-MAR-1999; 99US-0125359.
XX	PR 03-DEC-1999; 99US-016864.
PA	(GEST) GENSET.
XX	Dumas Milne Edwards J , Duclert A, Giordano J;
PT	DR ; 2000-500381/45.
XX	N-PSDB; C01529.
PT	New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNA and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
PT	PT
XX	Claim 13: SEQ ID 5604; 71pp + CD-ROM; English.
PS	XX
CC	The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
XX	Sequence 131 AA;
XX	Query Match 58.0%; Score 131; DB 21; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.4e-124;	
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
SQ	1 MGPLPRTVVELYDVSPLYSPWGLFEILCRYQNTWNINQLRPLSLITGIMKDSGNKPGLLP 60 1 mgplprtvelydvslpyswglfeilcrysinqntwninqlrplslitgimkdsgnkpgllp 60
Qy	61 RKGLYMANDLKLRRHLOQIPTHFPKDFLSVMLERGSLSLSMRFITAVNLHEPMLEKASRE 120 61 rkglymandlxlrrhloqiphpkdfsvmlerklsamrfitavnlhemlekasre 120
Db	61 1WMRVWSRNED 131 121 1WMRVWSRNED 131 121 1wmrvwsrnd 131
RESULT 4	ID B34972 Standard; Protein: 97 AA.
XX	XX
AC	B34972;
DT	26-JAN-2001 (first entry)
XX	XX
DE	Human secreted protein sequence encoded by gene 45 SEQ ID NO:176.
XX	XX
KW	Human; secreted protein; neuroprotective; cytotatic; cardioactive;
KW	immunomodulatory; muscular; pulmonary; gastrointestinal; nephrotropic;
KW	antinfective; gynaecological; gynaeological; antihelminthic; antiarthritic; neural disorder; cancer;
KW	immune disease; reproductive disorder; proliferative disorder;
KW	gastrointestinal disease; wound healing; infectious disease;
KW	anticonvulsant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW	hypotensive; dermatological; immunosuppressive; antinflammatory;
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW	antihaemolytic; gene therapy; cancer; proliferative disorder; hypertension;
XX	XX
RESULT 5	ID B43298
DT	08-FEB-2001 (first entry)
XX	XX
DE	Human ORF3062 polyptide sequence SEQ ID NO:61:24.
XX	XX
DE	Human ORF3062 polyptide sequence SEQ ID NO:61:24.
XX	XX
KW	Human; open reading frame; ORF3; detection; cytotatic; hepatotropic;
KW	antipsoratic; antiparkinsonian; nootropic; neuroprotective;
KW	osteopathic; antiarthritic; immunosuppressant; cardiant;
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW	hypotensive; dermatological; immunosuppressive; antinflammatory;
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW	antihaemolytic; gene therapy; cancer; proliferative disorder; hypertension;
PN	WO200056766-A1.
XX	XX

XX DT 02-NOV-2000 (first entry)
 XX DE Human Ma2 protein SEQ ID NO:7.
 XX
 AC B58191;
 XX DT 14-MAR-2001 (first entry)
 XX Lung cancer associated polypeptide sequence SEQ ID 529.
 DE Human; lung cancer associated protein; neuroprotective; cytostatic;
 KW cardiotropic; immunomodulatory; muscular active; vulnerable;
 KW gastrointestinal; nephrotropic; antiinfective; gynecological;
 KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
 KW proliferative disorder; wound healing; infectious disease.
 XX OS Homo sapiens.
 XX PN WO20055180-A2.
 XX PD 21-SEP-2000.
 XX PR 08-MAR-2000; 2000WO-US05918.
 XX PF 12-MAR-1999; 99US-0124270.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX PI Ruben SM;
 XX DR 2000-587514/55.
 DR N-PSDB; F18067.
 XX PT Lung cancer associated gene sequences, referred to as lung cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as lung cancer.
 XX PS Page 1021; 1425pp; English.
 XX PT Lung cancer associated gene sequences F17982 - F18424 encode human lung cancer
 CC associated proteins represented by B58106 - B58548. Lung cancer
 CC Polynucleotide sequences F17982 - F18424 encode human lung cancer
 CC associated proteins and Polynucleotide sequences, their agonists, and
 CC antagonists may have neuroprotective; cytostatic; cardioactive;
 CC immunomodulatory; muscular active general; pulmonary; gastrointestinal
 CC general; nephrotropic; antiinfective; gynecological; or antibacterial
 CC activity. The invention also includes antibodies specific for the protein
 CC or polynucleotide sequences. The lung cancer associated polynucleotide
 CC sequences may be used for detection of lung cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The proteins may be used to treat disorders such as
 CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
 CC cardiovascular, renal, and proliferative disorders. The proteins may also
 CC be used in the treatment of wounds and infectious diseases.
 CC Polynucleotide sequences F18425 - F18433 and peptide B58549 are used in
 CC the course of the invention for the identification and characterisation
 CC of the polynucleotide and protein sequences.
 XX SQ Sequence 179 AA;
 XX
 Query Match 3.5%; Score 8; DB 21; Length 179;
 Best Local Similarity 10.0%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 96 SLSAMRFL 103
 Db 25 slsamrfl 32
 RESULT 8
 B12526 ID B12526 standard; Protein: 195 AA.
 XX AC B12526;
 XX
 Query Match 3.5%; Score 8; DB 21; Length 195;
 Best Local Similarity 10.0%; Pred. No. 4.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 204 ELLAHLG 211
 Db 139 ellahlg 146
 RESULT 9
 B12528 ID B12528 standard; Protein: 283 AA.
 XX AC B12528;
 XX DT 02-NOV-2000 (first entry)
 XX DE Human Ma4 protein SEQ ID NO:11.
 KW Ma2; Ma3; Ma4; Ma5; paraneoplastic limbic encephalitis; diagnosis;
 KW paraneoplastic syndrome; neoplasm; colon cancer; brainstem encephalitis;
 KW breast cancer; parotid gland cancer; lung cancer; testicular cancer;
 KW germ-cell tumour.
 XX OS Homo sapiens.
 XX PN JP2000146982-A.

XX DR WPI; 1994-350275/44.
 XX DR N-PSDB; Q73061.
 XX PT Eliciting an immune response to *Salmonella* - using attenuated
 XX PT *Salmonella* strains, vector constructs, or componns. contng.
 XX PT fimbrial type proteins.
 XX Disclosure; Figure 2A-2D; 95pp; English.
 XX PS Disclosure; Figure 2A-2D; 95pp; English.
 XX CC The isolated SeFc protein may be used in a vaccine composition to
 CC elicit an immune response to *Salmonella* in animals (e.g. food
 CC producing animals) and humans.
 XX SQ Sequence 813 AA;
 XX Query Match 3.5%; Score 8; DB 15; Length 813;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 166 NQLKENTE 173
 Db 60 nqlkette 67
 RESULT 11
 W23573 W23573 standard; Protein; 814 AA.
 ID W23573 standard; Protein; 814 AA.
 XX AC W23573;
 XX DT 29-SEP-1997 (first entry)
 XX DE *Salmonella enteritidis* sefc.
 XX KW Enteropathogenic bacteria; *enterobacteria*; *S.enteritidis*; antibody.
 XX OS *Salmonella enteritidis*.
 XX PN US635617-A.
 XX PD 03-JUN-1997.
 XX PR 26-APR-1993; 93US-0054452.
 XX PR 26-APR-1993; 94US-0233788.
 XX PR 26-APR-1993; 93US-0054452.
 XX PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
 XX PI Clouthier SC, Collinson SK, Doran JL, Kay WH;
 XX DR WPI; 1997-309886/28.
 XX DR N-PSDB; T74143.
 XX Isolated *Salmonella* gene agfa - used for diagnosis of *Salmonella* or
 PT enteropathogenic bacteria of the *Enterobacteria* family
 XX Example 9; Fig 2; 85pp; English.
 XX
 XX The present sequence represents sefc found in the sef gene cluster
 CC from *Salmonella enteritidis*. The nucleic acid can be used to provide
 CC diagnostic assays for *Salmonella* and/or enteropathogenic bacteria of
 CC the family Enterobacteria. It can also be used to provide proteins and
 CC antibodies which can be used for assays. The nucleic acid sequence can
 CC be used to provide probes or primers which can specifically hybridise
 CC to nucleic acid molecules from greater than 99% of *Salmonella* strains
 CC that are pathogenic to warm-blooded animals relative to nucleic acid
 CC molecules from virtually all other microbial organisms.
 XX Sequence 814 AA;
 XX
 XX WO9425598 A.
 XX 10-NOV-1994.
 XX PD 26-APR-1994; 94WO-TB00207.
 XX PR 26-APR-1993; 93US-0054452.
 XX PA (KING J.) KING J. VICTORIA INNOVATION & DEV CORP.
 XX PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
 XX PI Clouthier SC, Collinson SK, Doran JL, Kay WH;
 XX DR WPI; 1997-309886/28.
 XX DR N-PSDB; T74143.
 XX Isolated *Salmonella* gene agfa - used for diagnosis of *Salmonella* or
 PT enteropathogenic bacteria of the *Enterobacteria* family
 XX Example 9; Fig 2; 85pp; English.
 XX
 XX The present sequence represents sefc found in the sef gene cluster
 CC from *Salmonella enteritidis*. The nucleic acid can be used to provide
 CC diagnostic assays for *Salmonella* and/or enteropathogenic bacteria of
 CC the family Enterobacteria. It can also be used to provide proteins and
 CC antibodies which can be used for assays. The nucleic acid sequence can
 CC be used to provide probes or primers which can specifically hybridise
 CC to nucleic acid molecules from greater than 99% of *Salmonella* strains
 CC that are pathogenic to warm-blooded animals relative to nucleic acid
 CC molecules from virtually all other microbial organisms.
 XX Sequence 814 AA;

FT sig-peptide 1..22
 XX OS Pseudomonas aeruginosa ATCC 33354 .
 PN EP357024-A.
 XX PD 07-MAR-1990.
 XX PF 30-AUG-1989; 89EP-0115992.
 XX PR 01-SEP-1988; 88DE-3829516.
 XX PA (BEHW) BEHRINGWERKE AG.
 XX PI Duchene M, von Specht U, Domdey H;
 DR WPI; 1990-068794/10.
 XX N-PSDB; Q03507.
 XX PT Pseudomonas aeruginosa outer membrane lipoprotein - useful for vaccine production.
 XX PB Example 5; Page 4; 5pp; German.
 XX CC and its fragments are useful for the production of vaccines and antisera against Pseudomonas infections. The DNA and antibodies are useful for diagnostic purposes.
 XX SQ Sequence 83 AA;

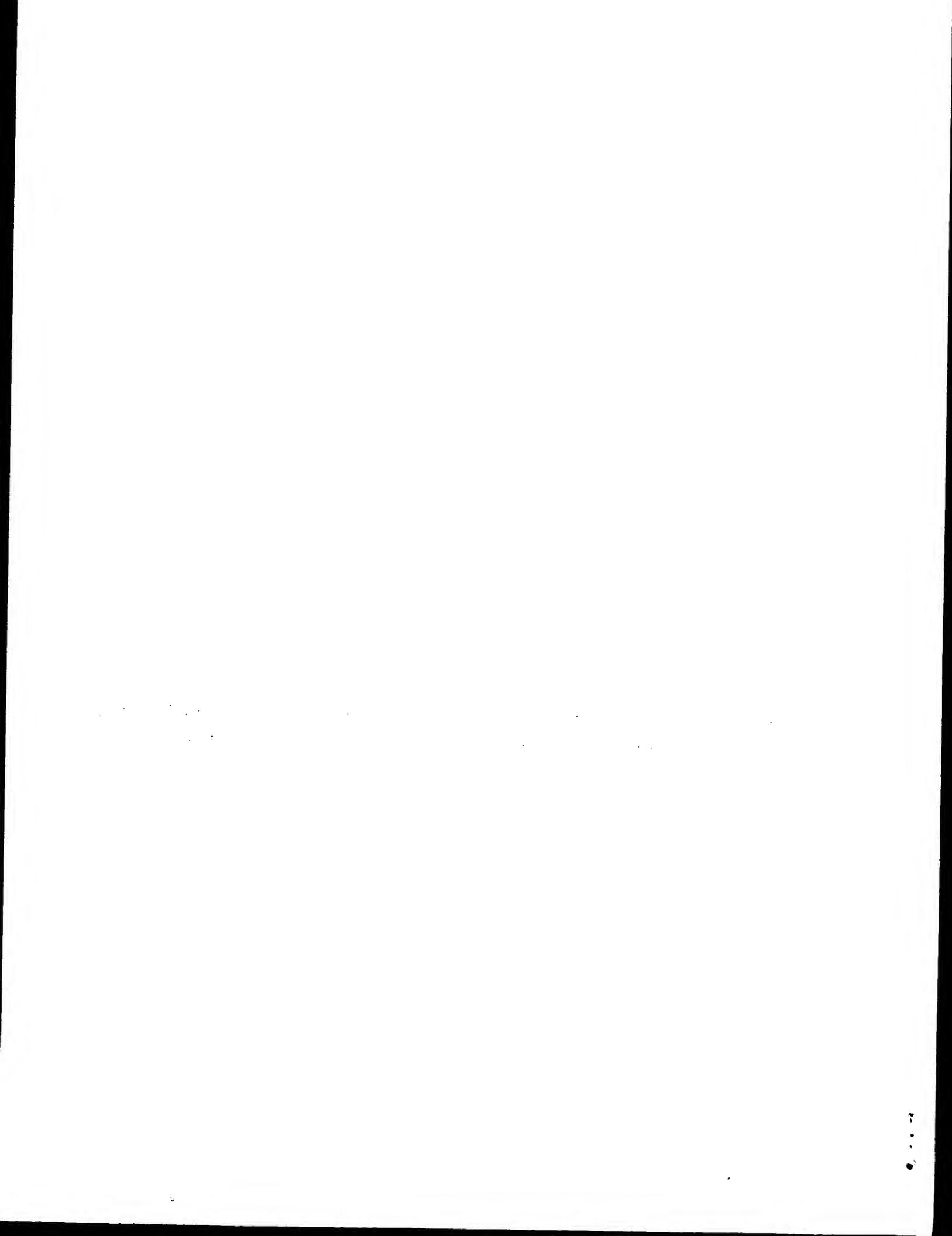
Query Match 3.1%; Score 7; DB 21; Length 130;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 113 MLEKASR 119
 Db 76 mlekasr 82

RESULT 15
 B58516 ID B58516 standard Protein: 130 AA.
 XX AC B58516;
 XX DT 14-MAR-2001 (first entry)
 XX DE Lung cancer associated polypeptide sequence SEQ ID 854.
 KW Human; lung cancer associated protein; neuroprotective; cytostatic;c;
 KW cardioactive; immunomodulatory; muscular active; vulnerable;
 KW gastrointestinal; nephrotropic; antinefertive; gynecological;
 KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
 KW proliferative disorder; wound healing; infectious disease.
 OS Homo sapiens.
 PN WO200055180-A2.
 XX PD 21-SEP-2000.
 XX PF 08-MAR-2000; 2000WO-US05918.
 XX PR 12-MAR-1999; 99US-0124270.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE-) ROSEN C A.
 XX PI Ruben SM;
 XX DR WPI; 2000-587514/55.
 DR N-PSDB; F18392.

XX PT Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer .
 XX PS Claim 11; Page 1391-1392; 1425pp; English.
 XX CC Polynucleotide sequences F17982 - F18124 encode human lung cancer associated proteins represented in B58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active; general; vulnerable; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. The peptides may also be used in the course of the invention for the identification and characterisation of the polynucleotide and protein sequences.
 XX SQ Sequence 130 AA;

Query Match 3.1%; Score 7; DB 21; Length 130;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 97 LSAMRFL 103
 Db 1 lsamrfl 7

Search completed: April 19, 2001, 12:58:35
 Job time: 113 sec



Matches	225;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	GPLPRTEVLFYDVLSPYSWLGFEILCRYONTWNINQLRPLSLITGIMKDSGNKPPGLLPR	61						Score 1.8; Best Local Similarity 100.0%; Pred. No. 9.9e-09; Mismatches 0; Conservative 16; Matches 225; Length 225;
Db	1	GPLPRTEVLFYDVLSPYSWLGFEILCRYONTWNINQLRPLSLITGIMKDSGNKPPGLLPR	60						
Qy	62	KGLYMANDKLRLRRHQIPIPHPKDFLSMILEKGSISAMREFLTAVNLHEPMLEKASEL	121						
Db	61	KGLYMANDKLRLRRHQIPIPHPKDFLSMILEKGSISAMREFLTAVNLHEPMLEKASEL	120						
RESULT	3	RECA_AQUPY	181	STANDARD;	PRT;	348 AA.			
Qy	122	WMRVWSRNEDITEPQSIIAAEKAGMSAQAGGLELKIAPKVKVNLQKETTEAACRYAF	180						
Db	121	WMRVWSRNEDITEPQSIIAAEKAGMSAQAGGLELKIAPKVKVNLQKETTEAACRYAF	180						
Qy	182	GLPITYAHVGOTHMLFGSDRMELLAHLGEKWMGPPIPAYNARL	226						
Db	181	GLPITYAHVGOTHMLFGSDRMELLAHLGEKWMGPPIPAYNARL	225						
RESULT	2	Aquifex_aquifilis	225	STANDARD;	PRT;	225 AA.			
Qy	GTAK1_RAT	AC009034;							
Qy	GTAK1_RAT	P2447;	01-MAR-1992	(Rel. 21, Created)					
Qy	GTAK1_RAT	DT15-JUL-1998	(Rel. 36, Last sequence update)						
Qy	GTAK1_RAT	DT01-OCT-2000	(Rel. 40, Last annotation update)						
Qy	GTAK1_RAT	DEGLUTATHIONE_S-TRANSFERASE	MITOCHONDRIAL (EC 2.5.1.18)	(GST 13-13)					
Qy	GTAK1_RAT	DEGSTK1	OR GSTK1-1.						
Qy	GTAK1_RAT	OSRattus norvegicus (Rat)	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Butelostomii; Mammalia; Eutheridia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
Qy	GTAK1_RAT	OCNCBI_TAXID=10116;							
Qy	GTAK1_RAT	RNRN	SEQUENCE FROM N.A.						
Qy	GTAK1_RAT	RPSEQUENCE FROM N.A.	TISSUE-Liver;						
Qy	GTAK1_RAT	RXMEDLINE#90709244; PubMed#8920976;							
Qy	GTAK1_RAT	RARHarris M.J.; Meyer D.J.; Coles B.; Ketterer B.; Pemble S.E.; Wardle A.F.; Taylor J.B.; A novel glutathione S-transferase class Kappa; characterization by the cloning of rat mitochondrial GST and identification of a human homologue.";							
Qy	GTAK1_RAT	RTBiochem. J. 278:137-141(1991).							
Qy	GTAK1_RAT	RT-1- FUNCTION: MIGHT CONFER PROTECTION AGAINST GENOTOXIC ELECTROPHILES IN THE MITOCHONDRIAL COMPARTMENT.							
Qy	GTAK1_RAT	RT-1- CATALYTIC ACTIVITY: RX + GLUTATHIONE = HX + R-S-GLUTATHIONE.							
Qy	GTAK1_RAT	RT-1- SUBUNIT: HOMODIMER.							
Qy	GTAK1_RAT	CC-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.							
Qy	GTAK1_RAT	CC-1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. KAPPA FAMILY.							
Qy	GTAK1_RAT	CC-SEQUENCE OF 1-33.							
Qy	GTAK1_RAT	RXMEDLINE#9135194; PubMed#1883325;							
Qy	GTAK1_RAT	RAHarris M.J.; Meyer D.J.; Coles B.; Ketterer B.; Pemble S.E.; Wardle A.F.; Taylor J.B.; A novel glutathione S-transferase (13-13) isolated from the matrix of rat liver mitochondria having structural similarity to class theta enzymes.";							
Qy	GTAK1_RAT	RTBiochem. J. 278:137-141(1991).							
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Qy	GTAK1_RAT	CC-1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. KAPPA FAMILY.							
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Qy	GTAK1_RAT	RXMEDLINE#9135194; PubMed#1883325;							
Qy	GTAK1_RAT	RAHarris M.J.; Meyer D.J.; Coles B.; Ketterer B.; Pemble S.E.; Wardle A.F.; Taylor J.B.; A novel glutathione S-transferase class Kappa; characterization by the cloning of rat mitochondrial GST and identification of a human homologue.";							
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Qy	GTAK1_RAT	RAHarris M.J.; Meyer D.J.; Coles B.; Ketterer B.; Pemble S.E.; Wardle A.F.; Taylor J.B.; A novel glutathione S-transferase class Kappa; characterization by the cloning of rat mitochondrial GST and identification of a human homologue.";							
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Qy	GTAK1_RAT	CC-SEQUENCE OF 1-33.							
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Gencore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.						
DM protein - protein search, using sw mode!						
Run on:	April 19, 2001, 12:58:57 ; Search time 10.12 Seconds (without alignments) 764.994 Million cell updates/sec					
title:	US-09-441-723-1					
perfect score:	226					
sequence:	1 MGPLRTVLEFYDVLSPSW					
scoring table:	AHLGEKWWGPIPPAVNARL 226					
OLIGO						
Gapop	60.0 , Gapext 60.0					
scoring table:						
searched:	93435 seqs, 34255486 residues					
word size :	0					
total number of hits satisfying chosen parameters:	93435					
minimum DB seq length:	0					
maximum DB seq length:	2000000000					
post-processing: Listing first 45 summaries						
database :	SwissProt_39:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
	8	Query	Score	Match	Length	ID
result	No.	Score				Description
1	225	99.6	225	1	GTK1_HUMAN	Q9Y93 homo sapien
2	16	7.1	225	1	GTK1_RAT	P24473 rattus norv
3	8	3.5	348	1	RECA_AQUPY	P23342 aquifex pyr
4	8	3.5	593	1	Y4OA_RHISN	P55586 rhizobium s
5	8	3.5	814	1	SEFC_SALEN	P33388 salmonella
6	7	3.1	71	1	RL29_RICPRA	P9293 riccia
7	7	3.1	83	1	MULI_PSEAE	P11221 pseudomonas
8	7	3.1	131	1	PROL_PHLPR	P35079 phleum prat
9	7	3.1	131	1	PRO2_PHLPR	P24650 phleum prat
10	7	3.1	131	1	PRO3_PHLPR	P24282 phleum prat
11	7	3.1	133	1	PROF_BETVE	P23816 betula verr
12	7	3.1	133	1	PROF_MBRAN	P49894 mercurialis
13	7	3.1	202	1	RS2_PYRHO	O59259 pyrrococcus
14	7	3.1	204	1	TD53_HUMAN	Q16890 homo sapien
15	7	3.1	204	1	TD53_MOUSE	P19493 ratus norv
16	7	3.1	354	1	YHL4_YEAST	P28780 sacharomyces
17	7	3.1	547	1	ODP2_PSEAE	P9638 pseudomonas
18	7	3.1	854	1	DDR2_MOUSE	Q62371 mus musculus
19	7	3.1	855	1	DDR2_HUMAN	Q16832 homo sapien
20	7	3.1	883	1	YHL6_YEAST	P28781 sacharomyces
21	7	3.1	902	1	GLR4_HUMAN	P19493 ratus norv
22	7	3.1	902	1	GLR4_RAT	P02455 sacharomyces
23	7	3.1	1875	1	MLP1_YEAST	Q9Z040 riccia
24	6	6	67	1	Y158_RICPRA	P00264 paracoccus
25	6	2.7	67	1	HPIS_PARSP	P81290 bacillus st
26	6	2.7	71	1	RS16_BACST	P56208 helicobac
27	6	2.7	93	1	RL23_HELPY	P21386 porphyra pu
28	6	2.7	118	1	FTRC_PORPU	P02366 bos taurus
29	6	2.7	127	1	NB4M_BOVIN	P66656 homo sapien
30	6	2.7	130	1	RS11_XANC	Q9Z3e9 xanthomonas
31	6	2.7	131	1	MY47_HUMAN	P924214 homo sapien
32	6	2.7	132	1	P14_HUMAN	P24473 rattus norv
33	6	2.7	132	1	P14_HUMAN	P24473 rattus norv

RESULT	1	RL14_HALMA
GTK1_HUMAN	ID	GTKL_HUMAN STANDARD;
AC	09Y2QJ; Q9P1S4;	PRT; 22
DT	01-OCT-2000 (Rel. 40, Created)	
DT	01-OCT-2000 (Rel. 40, Last annotation update)	
DT	01-OCT-2000 (Rel. 40, Last annotation update)	
DE	GLUTATHIONE S-TRANSFERASE, MITOCHONDRIAL	
DE	(GLUTATHIONE S-TRANSFERASE SUBUNIT 13)	
GN	GSTK1.	
OS	Homo sapiens (Human).	
OC	Mammalia; Eutheria; Chordata; Craniata;	
OC	Metazoa; Eutheria; Primates; Catarrhini;	
OX	NCBI_TAXID=9606;	
RN	[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Blood;	
RX	Medline=2499357; PubMed=11042152;	
RA	Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X.	
RA	Shen Y., Fan H.-Y., Lu G., Zhong M., Xu	
RA	Tao J., Huang Q.-H., Zhou J., Hu G.-X.	
RT	"Cloning and functional analysis of cDN	
RT	300 previously undefined genes expressed	
RT	stem/progenitor cells";	
RL	Genome Res. 10:1546-1560(2000).	
RN	[2]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	
RA	Zhao Z., Huang X., Li N., Zhu X., Cao X	
RT	"A novel gene from human dendritic cell	
RL	Submitted (MAY-1998) to the EMBL/Genbank	
CC	-!- FUNCTION: MIGHT CONFER PROTECTION AGAINST ELECTROPHILES IN THE MITOCHONDRIAL	
CC	-!- CATALYTIC ACTIVITY: RX + GLUTATHIONE	
CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY)	
CC	-!- SUBCELLULAR LOCATION: MITOCHONDRIAL	
CC	-!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY	
CC	This SWISS-PROT entry is copyright. It	
CC	between the Swiss Institute of Bioinformatics	
CC	and the European Bioinformatics Institute.	
CC	use by non-profit institutions as long	
CC	as this statement is not removed.	
CC	entities requires a license agreement (or	
CC	send an email to license@ebi.ac.uk)	
CC	EMBL; AR070657; AAD20963; -;	
DR	EMBL; AR068287; AAU65506; -;	
KW	Transferase; Mitochondrion.	
FT	INT-MET 0 0 BY SIMILAR	
FT	CONFICT 178 178 G > R (IN	
FT	CONFICT 219 219 G > S (IN	
SQ	SEQUENCE 225 AA: 25365 MW; FE91A5EE	

Db	2	NDLKLLR 8	
RESULT	7	MULI_PSEAE	SIGNAL
ID	P11221;	STANDARD	PRT;
AC	01-JUL-1989 (Rel. 11, Created)	83 AA.	
DT	01-JUL-1989 (Rel. 11, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	MAJOR OUTER MEMBRANE LIPOPROTEIN PRECURSOR (MUREIN-LIPOPROTEIN DE (LIPOPROTEIN I)).		
DE	OPIRI OR PA2853.		
GN	Pseudomonas aeruginosa.		
OS	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.		
OC	NCBI_TAXID=287;		
OX			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=TSOLATE PA2;		
RX	MEDLINE=891313294; PubMed=2473376;		
RA	Cornelius P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B., Hannert V., Hubert J.-C.;		
RA	"Cloning and analysis of the gene for the major outer membrane lipoprotein from <i>Pseudomonas aeruginosa</i> ."		
RT	Mol. Microbiol. 3:421-428(1989).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89327122; PubMed=2502533;		
RA	Duchene M., Barron C., Schweizer A., von Sprecht B.-J., Dondey H., RT cloning, sequence, and expression in <i>Escherichia coli</i> .";		
RT	J. Bacteriol. 171:4130-4137(1989).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 15692 / PAO1;		
RX	MEDLINE=92265853; PubMed=1588307;		
RA	Saint-Onge A., Romeyer F., Lebel P., Masson L., Brousseau R., RT specificity of the pseudomonas aeruginosa PAO1 lipoprotein I gene as a DNA probe and PCR target region within the Pseudomonadaceae.";		
RT	J. Gen. Microbiol. 138:733-741(1992).		
RL	[4]		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=PAO1;		
RX	MEDLINE=20437337; PubMed=10984043;		
RA	Stover C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltier L., Tolentino E., Westblom W.M., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbige K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.; RT "Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen."		
RT	Nature 406:958-964 (2000).		
RL	-		
CC	SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID ANCHOR.		
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CC			
DR	X13748; CAA32013..1; -;		
EMBL	M25761; AAA21880..1; -;		
EMBL	X58714; CAA41550..1; -;		
DR	A07695; CAA00707..1; -;		
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DR	SO4834; SO4834.. -;		
DR	X13748; CAA32013..1; -;		

DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 65.2 KDA PROTEIN Y4OA.
GN Y4OA, strain NGR234a.
OS Rhizobium sp.
OG Plasmid sym_PNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
NCBI_TaxID=394;
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97105956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC BIOSYNTHESIS PROTEIN MCGB.
-1 SIMILARITY: TO Y4QC.
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CC

DR AE00088; AAB91794.1; -.
DR InterPro: IPR00594; -.
DR PF00899; Thiel_Family; 1.
HYPOTHETICAL protein; Plasmid.
SEQUENCE 593 AA; 65216 MW; B6E248236AC9FF68C CRC64;
RN [1]
RP Query Match
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ QY 138 ILAAEKA 145
Db 242 ILAAEKA 249

RESULT 5
SEFC_SALEN STANDARD; PRT: 814 AA.
ID P3388;
AC 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
OUTER MEMBRANE USHER PROTEIN SEFC PRECURSOR.
GN Salmonella enteritidis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E; PubMed=9823893;
RX MEDLINE=99039499; RA Andersson J.O., Andersson S.G.E., Zomodoripour A., Podowski R.M., Naeslund A.K., Sicheritz-Ponten T., Alsmark U.C.M., Kurland C.G.;
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria";
RT Nature 396:133-140(1998).
RL -1 SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS.
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CC

EMBL: AJ235272; CAA15091.1; -.
DR InterPro: IPR001854; -.
DR Pfam: PF00831; Ribosomal_L29; 1;
DR PROSITE: PS00579; RIBOSOMAL_L29; 1.
KW Ribosomal protein.
SQ SEQUENCE 71 AA; 8406 MW; D3D06C34DA617C3E CRC64;
RN [1]
RP Query Match
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ QY 68 NDLLLR 74
CC |||||||

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CC

CC DR EMBL: L11010; AAC27221.1; -.
DR PIR: C40618; C40618.
DR InterPro: IPR00015; -.
DR Pfam: PF00577; Usher; 1.
DR PROSITE: PS01151; FIMBRIAL_USHER; FALSE_NEG.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 814 OUTER MEMBRANE USHER PROTEIN SEFC.
FT DISULFID 792 813 POTENTIAL.
SQ SEQUENCE 814 AA; 90.24 MW; AE7CC9D35C2FA0EB CRC64;

Query Match 3.5%; Score 8; DB 1; Length 814;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ QY 166 NQLKETTE 173
Db 60 NQLKETTE 67

RESULT 6
ID RL29_RICPCR STANDARD; PRT; 71 AA.
AC Q9ZCR3;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L29.
GN RPMC OR RP651.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsiidae; Rickettsia.
NCBI_TaxID=82;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E; PubMed=9823893;
RX MEDLINE=99039499; RA Andersson J.O., Andersson S.G.E., Zomodoripour A., Podowski R.M., Naeslund A.K., Sicheritz-Ponten T., Alsmark U.C.M., Kurland C.G.;
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria";
RT Nature 396:133-140(1998).
RL -1 SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS.

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CC

EMBL: AJ235272; CAA15091.1; -.
DR InterPro: IPR001854; -.
DR Pfam: PF00831; Ribosomal_L29; 1;
DR PROSITE: PS00579; RIBOSOMAL_L29; 1.
KW Ribosomal protein.
SQ SEQUENCE 71 AA; 8406 MW; D3D06C34DA617C3E CRC64;

Query Match 3.1%; Score 7; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ QY 68 NDLLLR 74
CC |||||||

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CC EMBL: AP000006; BAA30741..1; ALT_INIT.
 DR InterPro: IPR001865;
 DR Pfam: PF00318; Ribosomal_S2; 1.

DR PROSITE: PS0095; RIBOSOMAL_S2.
 DR PROSITE: PS00962; RIBOSOMAL_S2..1;
 DR PROSITE: PS00963; RIBOSOMAL_S2..2; 1.

KW Ribosomal protein.
 SQ SEQUENCE 202 AA; 23022 MW; 686F037D7AEFB57 CRC64;

Query Match 3.1%; Score 7; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No.13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 EP0SILA 140
 DR 63 EP0SILA 69

RESULT 14
 TPD53_HUMAN STANDARD; PRT; 204 AA.
 ID TD53_HUMAN STANDARD; PRT; 204 AA.
 AC Q16590;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR PROTEIN D53 (HD53) (D52-LIKE 1).
 GN TPDS2L1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxId=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE_Breast carcinoma;
 RX PubMed=97001154; Pubmed=8812487;
 RA Byrne J.A., Nourse C.R., Basset P.;
 RT "Definition of the tumor protein D52 (TPD52) gene family through
 cloning of D52 homologues in human (hd53) and mouse (md52)." ;
 RL Genomics 35:523-532(1996).

CC -!- SUBUNIT: FORMS HOMODIMER OR HETERO DIMER WITH OTHER MEMBERS OF THE
 CC FAMILY (BY SIMILARITY).
 CC !- SIMILARITY: BELONGS TO THE TPD52 FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC

CC DR EMBL: AF004428; ARQ98476.1; -.
 DR MGD: MGI:1298386; Tpd52I1.
 DR Coiled coil.
 FT DOMAIN 22 73 COILED COIL (POTENTIAL),
 SQ SEQUENCE 204 AA; 22515 MW; BAA49DAC7BF6BE8 CRC64;

Query Match 3.1%; Score 7; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No.13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 QAQGLE 157
 DR 4 QAQGLE 10

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 CC

CC DR EMBL: U44427; AAB0894..1; -.
 DR EMBL: U44428; AAB0895..1; -.
 DR MIM: 604069; -.
 RW Coiled coil.
 FT DOMAIN 22 73 COILED COIL (POTENTIAL),
 SQ SEQUENCE 204 AA; 22449 MW; 6B3C336D5C0653C9 CRC64;

Query Match 3.1%; Score 7; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No.13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 QAQGLE 157
 DR 4 QAQGLE 10

RESULT 15
 ID TD53_MOUSE STANDARD; PRT; 204 AA.
 AC 054818;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)

DE TUMOR PROTEIN D53 (MD53) (D52-LIKE 1).
 GN TPD52L1.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 OC NCBITaxId=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97001154; PubMed=8812487;
 RA Byrne J.A., Mattei M.-G., Basset P.;
 RT "Definition of the tumor protein D52 (TPD52) gene family through
 cloning of D52 homologues in human (hd53) and mouse (md52)." ;
 RL Genomics 35:523-532(1996).

CC -!- SUBUNIT: FORMS HOMODIMER OR HETERO DIMER WITH OTHER MEMBERS OF THE
 CC FAMILY (BY SIMILARITY).
 CC !- SIMILARITY: BELONGS TO THE TPD52 FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC

CC DR EMBL: AF004428; ARQ98476.1; -.
 DR MGD: MGI:1298386; Tpd52I1.
 DR Coiled coil.
 FT DOMAIN 22 73 COILED COIL (POTENTIAL),
 SQ SEQUENCE 204 AA; 22515 MW; BAA49DAC7BF6BE8 CRC64;

Query Match 3.1%; Score 7; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No.13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 QAQGLE 157
 DR 4 QAQGLE 10

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 CC

CC DR EMBL: U44427; AAB0894..1; -.
 DR EMBL: U44428; AAB0895..1; -.
 DR MIM: 604069; -.
 RW Coiled coil.
 FT DOMAIN 22 73 COILED COIL (POTENTIAL),
 SQ SEQUENCE 204 AA; 22449 MW; 6B3C336D5C0653C9 CRC64;

RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=97169442; PubMed=9016715;
 RA Fedorov A.A., Ball T., Mehoney N.M.; Valenta R., Almo S.C.;
 RT "The molecular basis for allergen cross-reactivity: crystal structure
 and IgE epitope mapping of birch pollen profilin."; crystal structure
 Structure 5:33-45(1997).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=97276803; PubMed=9130496;
 RA Fedorov A.A., Ball T., Valenta R., Almo S.C.;
 RT "X-ray crystal structures of birch pollen profilin and Phl p 2.";
 RL Int. Arch. Allergy Immunol. 113:109-113(1997).
 RN [4]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97415424; PubMed=9271223;
 RA Schomburg D., Jockusch B.M.;
 RT "Birch pollen profilin: structural organization and interaction with
 poly-(α -proline) peptides as revealed by NMR.";
 RT FEBS Lett. 411:291-295(1997).
 CC -!- FUNCTION: BINDS TO ACTIN AND AFFECTS THE STRUCTURE OF THE
 CC CYTOSKELETON. AT HIGH CONCENTRATIONS, PROFILIN PREVENTS THE
 CC POLYMERIZATION OF ACTIN, WHEREAS IT ENHANCES IT AT LOW
 CC CONCENTRATIONS. BY BINDING TO PIP2, IT INHIBITS THE FORMATION OF
 CC IP3 AND DG. (BY SIMILARITY).
 CC -!- SUBUNIT: OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC
 CC ACTIN IN A 1:1 RATIO.
 CC -!- DISEASE: CAUSE ALLERGIC REACTIONS.
 CC -!- SIMILARITY: BELONGS TO THE PROFILIN FAMILY.
 CC -----
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 CC -----
 EMBL; M65179; AA16522.1; -.
 CC -!- DISEASE: CAUSE ALLERGIC REACTIONS.
 CC -!- SIMILARITY: BELONGS TO THE PROFILIN FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR PIR; JC2082; JC2082.
 DR PDB; 1CQA; 1-FBP-97.
 DR InterPro; IPR00097; -.
 DR Pfam; PF00235; profilin; 1.
 DR PRINTS; PRO0392; PROFILIN.
 DR PROSITE; PS00414; PROFILIN; 1.
 DR Actin-binding; Cytoskeleton; Allergen; 3D-Structure.
 KW SEQUENCE 133 AA; 14253 MW; 9443FC43786EE11A CRC64;
 DR STRAIN=OT3; RC STRAIN=OT3;
 AC 049894; STANDARD; PRT; 133 AA.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DR 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PROFILIN (ALLERGEN MER A 1).
 OS Mercurialis annua (Annual mercury).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;
 OC Malpighiales; Euphorbiaceae; Mercurialis.
 OX NCBI_TAXID=3986;
 RN [1] SEQUENCE FROM N.A.
 RP -----
 RESULT 12
 PROF_MERAN STANDARD PRT; 133 AA.
 ID PROF_MERAN STANDARD PRT; 133 AA.
 AC 049894; STANDARD PRT; 133 AA.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DR 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PROFILIN (ALLERGEN MER A 1).
 OS Mercurialis annua (Annual mercury).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;
 OC Malpighiales; Euphorbiaceae; Mercurialis.
 OX NCBI_TAXID=3986;
 RN [1] SEQUENCE FROM N.A.
 RP -----
 TISSUE=Pollen; PubMed=955453;
 RX MEDLINE=98184365; PubMed=955453;
 RA Vallverdu A., Asturias J.A., Arilla M.C., Gomez-Bayon N., Martinez A.,
 RT "Characterization of recombinant Mercurialis annua major allergen Mer
 a 1 (profilin).";
 RT RL J. Allergy Clin. Immunol. 101:363-370(1998).
 CC -!- FUNCTION: BINDS TO ACTIN AND AFFECTS THE STRUCTURE OF THE
 CC CYTOSKELETON. AT HIGH CONCENTRATIONS, PROFILIN PREVENTS THE
 CC POLYMERIZATION OF ACTIN, WHEREAS IT ENHANCES IT AT LOW
 CC CONCENTRATIONS. BY BINDING TO PIP2, IT INHIBITS THE FORMATION OF
 CC IP3 AND DG (BY SIMILARITY).
 CC -!- SUBUNIT: OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC
 CC ACTIN IN A 1:1 RATIO.
 CC -!- DISEASE: CAUSE ALLERGIC REACTIONS.
 CC -!- SIMILARITY: BELONGS TO THE PROFILIN FAMILY.
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 CC -----
 EMBL; Y13271; CAA7720.1; -.
 DR InterPro; IPR02097; -.
 DR Pfam; PF00235; profilin; 1.
 DR PRINTS; PR00392; PROFILIN.
 DR PROSITE; PS00414; PROFILIN; 1.
 DR Actin-binding; Cytoskeleton; Allergen; SEQUENCE 133 AA; 14300 MW; 06D8C65.97217654F CRC64;
 SQ Query Match 3.1%; Score 7; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 9.1; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR QY 44 ITGIMKD 50
 DR Db 49 ITGIMKD 55
 DR RESULT 13
 DR RS2_PYRHO STANDARD; PRT; 202 AA.
 AC 059295; STANDARD; PRT; 202 AA.
 AC 059295; STANDARD; PRT; 202 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE 30S RIBOSOMAL PROTEIN S2P.
 GN RPS2 OR PH1629.
 OS Pyrococcus horikoshii.
 OC Archaea; Buryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
 OX NCBI_TAXID=53953; RN [1]
 RP SEQUENCE FROM N.A.
 RC -----
 RX MEDLINE=93344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Nagai Y.,
 RA Yamamoto S., Seine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamatsu M., Ohfukui Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaebacterium, Pyrococcus horikoshii On3.";
 RL DNA Res. 5:55-76(1998).
 CC -!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
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OM protein - protein search, using sw model

Run on: April 19, 2001, 12:57:26 ; Search time 15.56 Seconds
(without alignments).
998.161 Million cell updates/sec

Title: US-09-441-723-1
Perfect score: 226

Sequence: 1 MGPLPRTVELLYDVLSYWSW.....AHLGEKWNMGPIPPAVNRL 226

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 198801 seqs, 68722935 residues

Word size : 0

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_67;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

conserved hypothetical
hypothetical secret
methionyl-tRNA syn
hypothetical prote
tyro 10 receptor k
probable transcript
protein tyrosine k
glutamate receptor k
glutamate receptor k
probable RND efflu
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hypothetical prote
myosin-like prote
probable non-ribos
probable cell-surf
probable repressor

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	4.9	33	S17164	glutathione transf
2	8	3.5	77	C82988	hypothetical prote
3	8	3.5	305	T36056	recombination prot
4	8	3.5	348	A55020	fimbrial outer mem
5	8	3.5	814	C40618	ribosomal protein
6	7	3.1	71	A71671	outer membrane lpp
7	7	3.1	83	A33854	probable membrane
8	7	3.1	95	F81973	- common
9	7	3.1	131	JC2080	profilin - Europe
10	7	3.1	133	JC2082	probable chromosome
11	7	3.1	199	E75632	probable ribosomal
12	7	3.1	205	E71042	hypothetical prote
13	7	3.1	212	D70489	2-keto-3-deoxy-6-
14	7	3.1	220	G83247	hypothetical prote
15	7	3.1	251	T08315	probable bis(S,-nu
16	7	3.1	276	H81931	probable binding p
17	7	3.1	279	T36086	yeast atp12 prote
18	7	3.1	287	T39197	conserved hypothet
19	7	3.1	288	D82781	hypothetical prote
20	7	3.1	347	T14313	NADPH HC toxin red
21	7	3.1	357	T01434	cBD protein - Syn
22	7	3.1	364	S77360	conserved hypothet
23	7	3.1	376	B75260	hypothetical prote
24	7	3.1	376	E83604	probable pyridoxal
25	7	3.1	396	T27946	hypothetical prote
26	7	3.1	401	F83187	hypothetical prote
27	7	3.1	458	T34574	two-component syst
28	7	3.1	498	H82679	dihydrolipoamide a
29	7	3.1	547	H83018	

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probable repressor

QY	149	AEQAQGLL	156	J. Bacteriol. 175, 2523-2533, 1993
Db	65	AEQAQGLL	72	A;Title: Characterization of three fimbrial genes, <i>sefABC</i> , of <i>Salmonella enteritidis</i>
RESULT	3			
T36056				
C;Species: Streptomyces coelicolor				
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000				
C;Accession: T36056				
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.				
A;Reference number: 221595				
A;Accession: T36056				
A;Status: preliminary; translated from GB/EMBL/DDBJ				
A;Molecule type: DNA				
A;Residues: 1-305 <SNP>				
A;Cross-references: EMBL:AL034355; PIDN:CAAA22222.1; GSPDB:GN00070; SCOEDB:SCD78_17C				
A;Experimental source: strain A3 (2)				
C;Genetics:				
C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTTH10				
Query Match	3.5%	Score 8;	DB 2;	Length 305;
Best Local Similarity	100.0%	Pred. No. 2.9;		
Matches	8;	Conservative 0;	Mismatches 0;	Gaps 0;
QY	139	LAAREKAG	146	A71671 ribosomal protein L29 - <i>Rickettsia prowazekii</i>
Db	59	LAAREKAG	66	C;Species: <i>Rickettsia prowazekii</i> C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
RESULT	4			
A50200				
N;Alternate names: recombinant Aguifex pyrophilus				
C;Species: Aguifex pyrophilus				
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999				
C;Accession: A50200				
A;Status: preliminary; nucleic acid sequence not shown				
A;Molecule type: DNA				
A;Residues: 1-348 <NEW>				
A;Cross-references: GB:L23135; PIDN:9349396; PIDN:AAA67702.1; PID:9349397				
C;Keywords: ATP; DNA binding; DNA recombination; DNA repair; p-loop; SOS response				
F:71-78/Region: nucleotide-binding motif A (P-loop)				
F:145-150/Region: nucleotide-binding motif A (P-loop)				
P:77/Binding site: ATP (Lys) #status predicted				
Query Match	3.5%	Score 8;	DB 2;	Length 348;
Best Local Similarity	100.0%	Pred. No. 3.3;		
Matches	8;	Conservative 0;	Mismatches 0;	Gaps 0;
QY	108	LEHPMEME	115	A33854 outer membrane lipoprotein I precursor - <i>Pseudomonas aeruginosa</i>
Db	315	LEHPMEME	322	C;Species: <i>Pseudomonas aeruginosa</i> C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 31-Dec-2000
RESULT	5			
C40618				
C;Cross-references: GB:M25761; PIDN:9151334; PID:9151335				
R;Cornelis, P.; Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaeft, V.; Mol. Microbiol. 3, 421-428, 1989				
C;Species: <i>Salmonella enteritidis</i>				
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999				
C;Accession: C46118				
R;Cloutier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.				
Db				

A; Residues: 1-83 <COr>
A; Cross-references: EMBL:X13748; NID:945344; PIDN:CAA32013.1; PID:g45345
A; Note: the authors translated the codon GAA for residue 78 as Gly
A; Cross-references: GenBank:U00000000.1; NCBI:U00000000.1; PIDN:CAA1550.1; PID:g433510
A; Note: the authors translated the codon GAA for residue 78 as Gly
A; Title: Specificity of the *Pseudomonas aeruginosa* PAO1 lipoprotein I gene as a DNA probe
A; Reference number: A44834; MUID:92268853
A; Accession: A44834
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-83 <SAI>
A; Cross-references: GB:X58714; GB:S36066; NID:9433509; PIDN:CAA41550.1; PID:g433510
A; Experimental source: PAO1
A; Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBIPI:103667)
A; Cross-references: GenBank:U00000000.1; NCBI:U00000000.1; PIDN:CAA1550.1; PID:g433510
A; Note: the authors translated the codon GAA for residue 78 as Gly
A; Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen
A; Reference number: A82950; MUID:20437337
A; Accession: A82950
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-83 <SToR>
A; Cross-references: GB:AE004712; GB:AE004091; NID:g9948940; PIDN:AAG06241.1; GSPDB:GN001
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: oprf; PA2853
C; Keywords: lipid binding; lipoprotein; membrane protein
F; F:1-19/Doma1: signal sequence
F; F:20-83/Product: lipoprotein I
F; F:20-83/Predicted status: predicted
F; F:20-83/Domain: #status predicted
F; F:20-83/Protein: lipoprotein I
F; F:20-83/Genetics: MAT>

RESULT						
Query Match	3.1%	Score 7;	DB 2;	Length 83;		
Best Local Similarity	100.0%	Pred. No. 9.3;				
Matches	7;	Conservative	0;	Mismatches	0;	Gaps 0;
Oy	113	MLEKASR	119			
Db	76	MLEKASR	82			
RESULT						
F81873	8					
probable membrane protein NMA1081 [Imported]	-	Neisseria meningitidis (group A strain Z2)				
C;Species: Neisseria meningitidis						
C;Date: 05-May-2000 #sequence_revision 05-May-2000						
C;Accession: F81873						
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, i; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000						
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.						
A;Reference number: A81775; MUID:2022256						
A;Accession: F81873						
A;Status: Preliminary						
A;Molecule type: DNA						
A;Residues: 1-95 <PAR>						
A;Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CAB84344.1; PID:9737977/						
A;Experimental source: serogroup A, strain Z2491						
C;Genetics:						
A;Gene: NMA1081						
RESULT						
Query Match	3.1%	Score 7;	DB 2;	Length 95;		
Best Local Similarity	100.0%	Pred. No. 11;				
Matches	7;	Conservative	0;	Mismatches	0;	Gaps 0;
Oy	44	ITGIMKD	50			
Db	59	ITGIMKD	65			

JC2080 common timothy
 profilin - common timothy
 N;Alternate names: actin-binding protein
 C;Species: Phleum pratense (common timothy)
 C;Date: 14-Jul-1994 #text_change 13-Aug-1999
 C;Revision: 14-Jul-1994 #sequence_revision 14-Jul-1994
 C;Accession: JC2080; S4023
 R;Valenta, R.; Ball, T.; Virtala, S.; Duchene, M.; Kraft, D.; Scheiner, O.
 Biochim. Biophys. Res. Commun. 1994, 199, 106-118.
 A;Title: cDNA cloning and expression of timothy grass (*Phleum pratense*) pollen proteins
 A;Reference number: JC2080; MUID:94168560
 A;Accession type: JC2080
 A;Molecule type: mRNA
 A;Residues: 1-131 <VAL>
 A;Cross-references: EMBL:X77583; PIDN:CAA54686.1; PID:9453976
 A;Experimental source: pollen
 C;Superfamily: profilin
 C;Keywords: actin binding; cytoskeleton

Query Match	3.1%	Score 7;	DB 2;	Length 131;	
Best Local Similarity	100.0%	Pred. No. 14;			
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy 44	ITGIMKD 50				
Db 47	ITGIMKD 53				
RESULT 10					
JC2082	profilin - European white birch				
N;Alternate names: actin-binding protein					
C;Species: Betula pendula (European white birch)					
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 17-Mar-1999					
C;Accession: JC2082					
R;Valenta, R.; Ball, T.; Virtala, S.; Duchene, M.; Kraft, D.; Scheiner, O.					
Biochem. Biophys. Res. Commun. 199, 106-118, 1994					
A;Title: cDNA cloning and expression of timothy grass (<i>Phleum pratense</i>) pollen proteins					
A;Reference number: JC2080; MUID:94168560					
A;Accession: JC2082					
A;Molecule type: mRNA					
A;Residues: 1-133 <VAL>					
A;Experimental source: pollen					
C;Comment: This protein is responsible for cross-reactivities in 20% of pollen antibodies					
C;Superfamily: profilin					
C;Keywords: actin binding; cytoskeleton					
Query Match	3.1%	Score 7;	DB 2;	Length 133;	
Best Local Similarity	100.0%	Pred. No. 15;			
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy 44	ITGIMKD 50				
Db 49	ITGIMKD 55				
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E75637	Probable chromosome partitioning protein Para family - Deinococcus radiodurans				
C;Species: Deinococcus radiodurans					
C;Accession: E75637					
R;White, O.; Eisen, J.A.; Heldelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, S.J.; Smith, H.O.; Venter, J.C.; Fraser, C.M.					
Science 286, 1571-1577, 1999					
A;Title: Genome sequence of the radioresistant bacterium <i>Deinococcus radiodurans</i>					
A;Reference number: A75250; MUID:20036896					
A;Accession: E75637					
A;Status: preliminary					
A;Molecule type: DNA					
A;Residues: 1-199 <WHI>					

A;Cross-references: GB:AE001627; NID:96460959; PID:AAF12679.1; TIGR:DRC00
 A;Experimental source: strain RI
 C;Genetics:
 R;Gene: DRC0025
 R;Map position: plasmid
 R;Genome: plasmid
 R;Note: Plasmid CP1

Query Match 3.1%; Score 7; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 37 LQLRPSL 43
 Db 130 LQLRPSL 136

RESULT 12
 E71042 probable ribosomal protein S2 - Pyrococcus horikoshii.
 C;Species: Pyrococcus horikoshii
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 18-Aug-2000
 C;Accession: E71042
 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohfukui, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.;NIA Res. 5, 55-16, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon.
 A;Reference number: A71000; MUID:98344137
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-205 <RAW>
 A;Cross-references: GB:AP000006; NID:93236133; PID:BAA30741.1; PID:g3258058
 A;Experimental source: strain OR3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH1629
 C;Superfamily: yeast ribosomal protein S1.e

Query Match 3.1%; Score 7; DB 2; Length 205;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 134 EP0SILA 140
 Db 66 EPQSIL 72

RESULT 13
 D70489 hypothetical protein aq_2203 - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
 C;Accession: D70489
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovatur, Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyper-thermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:98196666
 A;Accession: D70489
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-212 <AQF>
 A;Cross-references: GB:AE000777; NID:92984377; PID:AAC07907.1; PID:g2984389; GB:AE000655
 A;Experimental source: strain VF5
 C;Genetics:
 A;Gene: aq_2203
 C;Superfamily: Aquifex aeolicus hypothetical protein aq_2203

Query Match 3.1%; Score 7; DB 2; Length 212;

Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 14
 G83247 2-keto-3-deoxy-6-phosphogluconate aldolase PA3181 [Imported] - Pseudomonas aeruginosa
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: G83247
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.Y.; Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic
 A;Reference number: A82250; MUID:20437337
 A;Accession: G83247
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-220 <STO>
 A;Cross-references: GB:AE004742; GB:AE004091; NID:9949294; PIDN:AAG06569.1; GSPDB
 A;Experimental source: strain PAO1
 C;Genetics:
 A;Gene: PA3181
 C;Superfamily: 2-dehydro-3-deoxyphosphogluconate aldolase

Query Match 3.1%; Score 7; DB 2; Length 220;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 140 AAAEKAG 146
 Db 84 AAAEKAG 90

RESULT 15
 T08315 hypothetical protein H1185 [Imported] - Halobacterium sp. (strain NRC-1) plasmid pS1
 C;Species: Halobacterium sp.
 A;Variety: strain NRC-1
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Nov-2000
 C;Accession: T08315
 R;Ng, W.V.; Clouto, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, Genome Res., 8, 1131-1141, 1998
 A;Title: Snapshot of a large dynamic replicon in a halophilic archaeon: megaplasmid
 A;Reference number: Z16408; MUID:919063795
 A;Accession: T08315
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-51 <DAS>
 A;Cross-references: EMBL:AF016485; NID:92822278; HALOSP:H1185
 A;Experimental source: strain NRC-1
 C;Genetics:
 A;Gene: HALOSP:H1185
 A;Genome: Plasmid pNRC100
 C;Superfamily: Halobacterium plasmid pNRC100 hypothetical protein H1185

Query Match 3.1%; Score 7; DB 2; Length 251;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

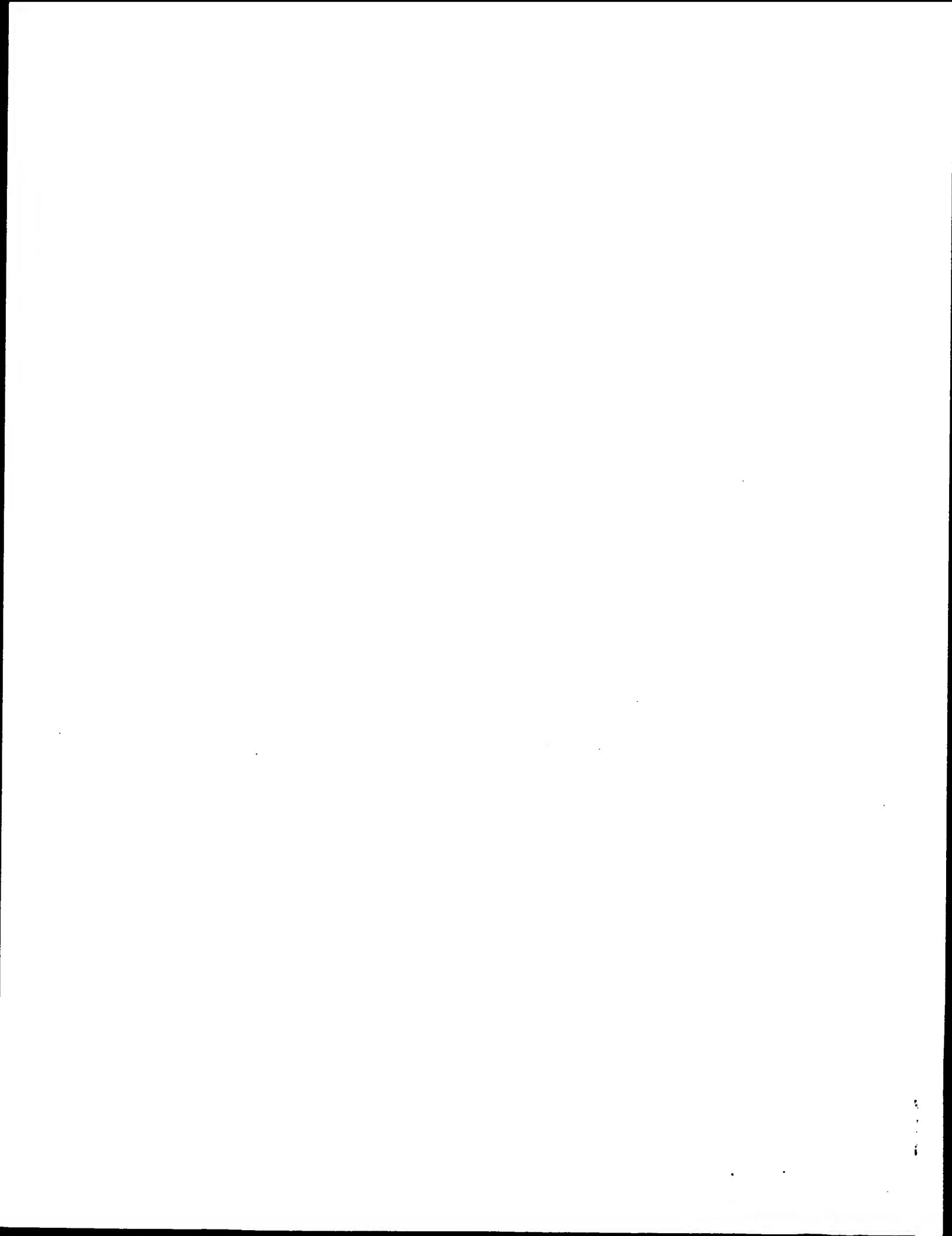
Qy 204 ELLAHL 210
 Db 64 ELLAHL 70

Fri Apr 20 10:52:39 2001

us-09-441-723-1.rpr

Page 5

Search completed: April 19, 2001, 12:59:14
Job time: 108 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
OM_protein - protein search, using sw model
Run on: April 19, 2001, 12:57:21 ; Search time 14.05 Seconds
(without alignments)
309.014 Million cell updates/sec

Title: US-09-441-723-1
Perfect score: 226
Sequence: 1 MCPLPRTVLFYDYLSPYSW.....AHLIGEKWMGGPIPPAYNARL 226

Scoring table: OLI00 Gapop 60.0 , Gapext 60.0

Searched: 185757 seqs, 19210857 residues

Word size : 0

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cgn2_6/ptodata/2/1aa/5A_COMB_pep:
 2: /cgn2_6/ptodata/2/1aa/5B_COMB_pep:
 3: /cgn2_6/ptodata/2/1aa/6A_COMB_pep:
 4: /cgn2_6/ptodata/2/1aa/6B_COMB_pep:
 5: /cgn2_6/ptodata/2/1aa/PCUTUS_COMB_pep:
 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	226	100.0	226	US-09-978-174-1
2	16	7.1	226	US-09-978-174-3
3	8	3.5	814	US-09-933-788A-42
4	7	3.1	63	US-08-577-447C-9
5	7	3.1	131	US-07-846-932-11
6	7	3.1	131	US-08-469-555-11
7	7	3.1	133	US-07-846-992-3
8	7	3.1	133	US-08-649-555-3
9	7	3.1	204	US-08-115-204-1
10	7	3.1	204	US-08-691-814B-10
11	7	3.1	204	US-09-162-597-1
12	7	3.1	214	US-08-972-447C-13
13	7	3.1	221	US-09-031-563-22
14	7	3.1	226	US-08-572-447C-15
15	7	3.1	291	US-08-987-379-14
16	7	3.1	291	US-08-987-379-16
17	7	3.1	685	US-09-031-563-21
18	7	3.1	854	US-08-056-647B-20
19	7	3.1	854	US-08-237-401A-20
20	7	3.1	855	US-08-936-347A-4
21	7	3.1	902	US-07-718-575-8
22	7	3.1	902	US-08-259-164-2
23	7	3.1	902	US-08-981-206-8
24	7	3.1	902	US-08-986-269A-8
25	7	3.1	1055	US-09-031-563-27
26	7	3.1	1315	US-09-031-563-2
27	7	3.1	1315	US-09-031-563-25

ALIGNMENTS

RESULT 1
US-09-441-723-1
; Sequence 1, Application US/08978174
; Patent No. 6030809
; GENERAL INFORMATION:
; APPLICANT: Shah, Purvi J.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW GLUTATHIONE-S-TRANSFERASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978-174
; FILING DATE: Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0430 US
; PRIORITY APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0430 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT04
; CLONE: 1554593
; US-08-978-174-1

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 Best Local Similarity 100.0%; Pred. No. 4.5e-223; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MGPLPRTVELFDVLSPIWGLPPIKQYQINNINQLRPSLITGIMKSGNPKPGLLP 60

Qy 61 RKGLYMANDLKLLRHHLQIPHFPKDFLSVMLKGSLSAMRELTAVNLHEPMLEKASRE 120
 Db 61 RKGLYMANDLKLLRHHLQIPHFPKDFLSVMLKGSLSAMRELTAVNLHEPMLEKASRE 120

Qy 121 LMWRYWSRNEDTEPOSTILAEEKAGNSAEOAQGLEKTATPKVKNQLEKTTAACRYGA 180
 Db 121 LMWRYWSRNEDTEPOSTILAEEKAGNSAEOAQGLEKTATPKVKNQLEKTTAACRYGA 180

Qy 181 FGLPTVAHVHDQTHMFLFGSDRMELLAHLGEKWMGPPIPPAVNRL 226
 Db 181 FGLPTVAHVHDQTHMFLFGSDRMELLAHLGEKWMGPPIPPAVNRL 226

RESULT ³
 US-08-233-788A-42 ; Sequence 42, Application US/08233788A
 ; Patent No. 563617
 ; GENERAL INFORMATION:
 ; APPLICANT: Doran, James L.
 ; APPLICANT: Kay, William W.
 ; APPLICANT: Cloutier, Sharon C.
 ; APPLICANT: Collinson, Karen S.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: U.S.A.
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/233,788A
 ; FILING DATE: 26-APR-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: King, Joshua
 ; REGISTRATION NUMBER: 35,570
 ; REFERENCE/DOCKET NUMBER: 920043, 403C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; TELEX: 3723816 SEEDANBERRY
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 814 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-233-788A-42

RESULT ⁴
 US-08-572-447C-9 ; Sequence 9, Application US/08572447C
 ; Patent No. 5955090
 ; GENERAL INFORMATION:
 ; APPLICANT: Knapp, Bernhard
 ; APPLICANT: Hungerer, Klaus-Dieter
 ; APPLICANT: Broker, Michael
 ; APPLICANT: Von Specht, Bernd-Ulrich
 ; APPLICANT: Domdey, Horst
 ; TITLE OF INVENTION: Immunogenic Hybrid Protein Oprf-Opri
 ; Derived From Pseudomonas aeruginosa Membrane Proteins.

Query Match 7.1%; Score 16; DB 3; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08; Mismatches 0; Indels 0; Gaps 0;

Qy 166 NQLKETTE 173
 Db 60 NQLKETTE 67

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 Best Local Similarity 100.0%; Pred. No. 5.9; Mismatches 0; Indels 0; Gaps 0;

Qy 166 NQLKETTE 173
 Db 60 NQLKETTE 67

NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/572,447C
 FILING DATE: 14-DEC-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94120023.0
 FILING DATE: 16-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: M. Paul Barker
 REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 05552.1395-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 63 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-572-447C-9

Query Match Best Local Similarity 100.0%; Score 7; DB 2; Length 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-07-846-992-11
 Sequence 11, Application US/07846992
 ; GENERAL INFORMATION:
 ; APPLICANT: Valentia, Rudolf
 ; APPLICANT: Duchene, Michael
 ; APPLICANT: Pettenburger, Karin
 ; APPLICANT: Breitenbach, Michael
 ; APPLICANT: Kraft, Dietrich
 ; APPLICANT: Rumpold, Helmut
 ; APPLICANT: Scheiner, Otto
 ; TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/846,992
 FILING DATE: 19-NOV-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/353,844
 FILING DATE: 18-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Jones III, Harry C
 REGISTRATION NUMBER: 20,280
 REFERENCE/DOCKET NUMBER: 6530-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 863-9099
 TELEFAX: (212) 863-8864/9741
 TELEX: 66141 PENNTE 11:
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 131 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Phleum pratense
 FEATURE:
 OTHER INFORMATION: Amino acid identity with P14
 OTHER INFORMATION: allergen from Betula verrucosa is 77%
 US-07-846-992-11

Query Match Best Local Similarity 100.0%; Score 7; DB 1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 ITGIMKD 50
 Db 47 ITGIMKD 53

RESULT 6
 US-08-469-555-11
 Sequence 11, Application US/08469555
 ; GENERAL INFORMATION:
 ; APPLICANT: Valentia, Rudolf
 ; APPLICANT: Duchene, Michael
 ; APPLICANT: Pettenburger, Karin
 ; APPLICANT: Breitenbach, Michael
 ; APPLICANT: Kraft, Dietrich
 ; APPLICANT: Rumpold, Helmut
 ; APPLICANT: Scheiner, Otto
 ; TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; APPLICATION NUMBER: US/08/469,555
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/846,992
 ; FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US/07/353, 844
 FILING DATE: 18-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Jones III, Harry C
 REGISTRATION NUMBER: 20, 280
 REFERENCE/DOCKET NUMBER: 6530-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Betula verrucosa

FEATURE: Amino acid sequence identity
 OTHER INFORMATION: With profilin of other organisms is as follows:
 OTHER INFORMATION: 30% with human profilin, 28% with calf and mouse,
 OTHER INFORMATION: 26% with yeast and 25% with Acanthamoeba
 US-07-846-992-3

OTHER INFORMATION: Amino acid identity with P14
 OTHER INFORMATION: Allergen from Betula verrucosa is 77%
 US-08-469-555-11

Query Match 3.1%; Score 7; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 44 ITGIMKD 50
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 US-08-469-555-3

US-07-846-992-3

Sequence 3, Application US/08469555
 Patent No. 5648242

GENERAL INFORMATION:
 APPLICANT: Valenta, Rudolf
 APPLICANT: Duchene, Michael
 APPLICANT: Pettenburger, Karin
 APPLICANT: Breitenbach, Michael
 APPLICANT: Kraft, Dietrich
 APPLICANT: Rumpold, Helmut
 APPLICANT: Scheiner, Otto
 TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/846, 992
 FILING DATE: 19920606
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/353, 844
 FILING DATE: 18 MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Jones III, Harry C
 REGISTRATION NUMBER: 20, 280
 REFERENCE/DOCKET NUMBER: 6530-011
 TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Betula verrucosa

FEATURE: Amino acid sequence identity
 OTHER INFORMATION: with profilin of other organisms is as follows:
 OTHER INFORMATION: 30% with human profilin, 28% with calf and mouse,
 OTHER INFORMATION: 26% with yeast and 25% with Acanthamoeba

US-08-469-555-3

Query Match 3.1%; Score 7; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 QAQGLE 157
 Db 4 QAQGLE 10

RESULT 10
 US-08-691-814B-10
 Sequence 10, Application US/08691814B
 Patent No. 5981218

GENERAL INFORMATION:
 APPLICANT: Rio, Marie-Christine
 APPLICANT: Tomasetto, Catherine
 APPLICANT: Basset, Paul
 APPLICANT: Byrne, Jennifer

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
 TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Ave., NW, Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/691,814B
 FILING DATE: 31-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/002,183
 FILING DATE: 09-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Steffe, Eric K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1383.0090001

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-691-814B-10

RESULT 9
 US-08-715-204-1
 Sequence 1, Application US/08715204
 Patent No. 5874286

GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Au-Young, Janice
 APPLICANT: Golik, Surya K.
 APPLICANT: Hiliman, Jennifer
 APPLICANT: Zweiger, Gary B.

TITLE OF INVENTION: A NOVEL TUMOR PROTEIN

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/715,204
 FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 6,749
 REFERENCE/DOCKET NUMBER: PF-0126 US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE: Consensus

RESULT 11
 US-09-162-597-1
 Sequence 1, Application US/09162597
 Patent No. 6043343

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
 APPLICANT: Au-Young, Janice
 APPLICANT: Goli, Surya K
 APPLICANT: Hillman, Jennifer.
 APPLICANT: Zweiiger, Gary B.

TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
 NUMBER OF SEQUENCES: 7

ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/162,597
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/715,204
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REFERENCE/DOCKET NUMBER: PF-0126 US
 TELEPHONE: 415-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 TELEFAX: 415-555-0555
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE: Consensus
 US-09-162-597-1

Query Match 3.1%; Score 7; DB 3;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 151 QAGGLE 157
 Db 4 QAGGLE 10

RESULT 12
 US-08-572-447C-13

GENERAL INFORMATION:
 Patent No. 5955090
 .GENERAL INFORMATION:
 Knapp, Bernhard
 APPLICANT: Knapp, Bernhard
 Hungerer, Klaus-Dieter
 APPLICANT: Hungerer, Klaus-Dieter
 Broker, Michael
 APPLICANT: Broker, Michael
 Von Specht, Bernd-Ulrich
 APPLICANT: Von Specht, Bernd-Ulrich
 Domdey, Horst
 APPLICANT: Domdey, Horst
 TITLE OF INVENTION: Immunogenic Hybrid Protein OprE-OprI
 TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington D.C.
 STATE: D.C.

COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/572,447C
 FILING DATE: 14-DEC-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94120023.0
 FILING DATE: 16-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: M. Paul Barker
 REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 05552.1395-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 214 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-572-447C-13

Query Match 3.1%; Score 7; DB 2;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 113 MLEKASR 119
 Db 207 MLEKASR 213

RESULT 13
 US-09-031-563-22
 Sequence 22, Application US/09031563A
 ; GENERAL INFORMATION:
 ; APPLICANT: Arnon Rosenthal
 ; Patent No. 6022708
 ; TITLE OF INVENTION: Fused
 ; FILE REFERENCE: P1272
 ; CURRENT APPLICATION NUMBER: US/09/031,563A
 ; CURRENT FILING DATE: 1998-02-26
 ; NUMBER OF SEQ ID NOS: 27
 ; SEQ ID NO 22
 ; LENGTH: 221
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-031-563-22

Query Match 3.1%; Score 7; DB 3;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 38 QLRPSLI 44
 Db 66 QLRPSLI 72

RESULT 14
 US-08-572-447C-15
 Sequence 15, Application US/08572447C
 ; Patent No. 5955090
 ; GENERAL INFORMATION:
 ; APPLICANT: Knapp, Bernhard

APPLICANT: Hungerer, Klaus-Dieter
 APPLICANT: Broker, Michael
 APPLICANT: Von Specht, Bernd-Ulrich
 APPLICANT: Domdey, Horst
 TITLE OF INVENTION: Immunogenic Hybrid Protein OptF-Opori
 TITLE OF INVENTION: Derived From *Pseudomonas aeruginosa* Membrane Proteins.
 NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner
 STREET: 1300 I Street, N.W., Suite 700

CITY: Washington
 STATE: D.C.
 COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/572,447C

FILING DATE: 14-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 941200023.0

FILING DATE: 16-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: M. Paul Barker

REGISTRATION NUMBER: 32,013

REFERENCE/DOCKET NUMBER: 05552.1395-000000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 226 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-572-447C-15

Query Match Score 7; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 MLEKASR 119
 |||||
 Db 56 MLEKASR 62

RESULT 15
 US-08-687-379-14

; Sequence 14, Application US-08687379
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoeger, Thomas
 ; APPLICANT: Ultsch, Andreas
 ; APPLICANT: Bach, Alfred
 ; APPLICANT: Sterrer, Sylvia
 ; APPLICANT: Lemaire, Hans-Georg

; TITLE OF INVENTION: Subunits of Glutamate Receptors, Their Preparation and Their Use

; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Keil & Weinkauf

; STREET: 1101 Connecticut Avenue
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036
 ; COMPUTER READABLE FORM:

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: April 19, 2001, 12:58:37 ; Search time 24.77 Seconds
(without alignments)
1069.398 Million cell updates/sec

Title: US-09-441-723-1
Perfect score: 226
Sequence: 1 MGPLPRTVELFYDVLSPSW.....AHLGEKWNMGPIPPAVNARL 226

Scoring table: Oligo Gapext 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 0

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTRMBL15:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_unclassified:
 13: sp_vertebrate:
 14: sp_virus:
 15: sp_worm:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8 Query Match Length DB ID Description
 1 226 100 0 226 4 Q9Y2Q3 homo sapien
 2 178 78.8 226 4 Q9P1S4 homo sapien
 3 8 3.5 283 4 Q9UJ42 homo sapien
 4 8 3.5 305 2 Q9BY2 streptomyces
 5 8 3.5 364 4 Q94959 homo sapien
 6 8 3.5 392 13 Q9TBFO arguilla ja
 7 8 3.5 419 13 Q9PUT7 brachydani
 8 8 3.5 426 13 Q9W61.1 cynops pyrr
 9 7 3.1 83 2 Q85409 pseudomonas
 10 7 3.1 83 2 Q85410 pseudomonas
 11 7 3.1 83 2 Q85411 pseudomonas
 12 7 3.1 83 2 Q85412 pseudomonas
 13 7 3.1 83 2 Q85413 pseudomonas
 14 7 3.1 83 2 Q85414 pseudomonas
 15 7 3.1 83 2 Q85415 pseudomonas
 16 7 3.1 83 2 Q85416 pseudomonas
 17 7 3.1 83 2 Q85417 pseudomonas
 18 7 3.1 83 2 Q85418 pseudomonas
 19 7 3.1 83 2 Q85419 pseudomonas

Result No.	Score	Query Match	Length	DB	ID	Description
1	226	100	0	226	4	Q9Y2Q3 homo sapien
2	178	78.8	226	4	Q9P1S4 homo sapien	Q9p1s4 homo sapien
3	8	3.5	283	4	Q9UJ42 homo sapien	Q9uJ42 homo sapien
4	8	3.5	305	2	Q9BY2 streptomyces	Q9by2 streptomyces
5	8	3.5	364	4	Q94959 homo sapien	Q94959 homo sapien
6	8	3.5	392	13	Q9TBFO arguilla ja	Q9tbfo arguilla ja
7	8	3.5	419	13	Q9PUT7 brachydani	Q9put7 brachydani
8	8	3.5	426	13	Q9W61.1 cynops pyrr	Q9w61.1 cynops pyrr
9	7	3.1	83	2	Q85409 pseudomonas	Q85409 pseudomonas
10	7	3.1	83	2	Q85410 pseudomonas	Q85410 pseudomonas
11	7	3.1	83	2	Q85411 pseudomonas	Q85411 pseudomonas
12	7	3.1	83	2	Q85412 pseudomonas	Q85412 pseudomonas
13	7	3.1	83	2	Q85413 pseudomonas	Q85413 pseudomonas
14	7	3.1	83	2	Q85414 pseudomonas	Q85414 pseudomonas
15	7	3.1	83	2	Q85415 pseudomonas	Q85415 pseudomonas
16	7	3.1	83	2	Q85416 pseudomonas	Q85416 pseudomonas
17	7	3.1	83	2	Q85417 pseudomonas	Q85417 pseudomonas
18	7	3.1	83	2	Q85418 pseudomonas	Q85418 pseudomonas
19	7	3.1	83	2	Q85419 pseudomonas	Q85419 pseudomonas

RESULT ID	1	PRELIMINARY;	PRT;	226 AA.
09Y2Q3				
AC	Q9Y2Q3;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	GLUTATHIONE S-TRANSFERASE SUBUNIT 13 HOMOLOG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Mao M., Ye M., Zhang Q., Zhou J., Wu J., Shen Y., Kan L., He K., Gu B., Fu G., Chen S., Chen Z.;			
RA	"Human rGSTK1-1 homolog gene."			
RT	Submitted (JUN-1998) to the EMBL/GenBank/DDJB databases.			
RL	EMBL; AF070657; AAD20963.1; -.			
DR	KW Transferase.			
SQ	SEQUENCE 226 AA; 25497 MW; D3FDADF1533B58A4 CRC64;			

Query Match	Length	DB	ID	Score	226:	DB 4:	Length 226:
Best Local Similarity				100.0%	100.0%	DB 4:	Length 226:
Matches	226:	Conservative	0:	Mismatches	0:	Indels	0:
							Gaps 0:
Qy	1	MGPLPRTVELFVDSLPSWLGIELCRYQNIWNTNLQRPLSLTGIMKDSCKPKPLGP	L	60			
Db	1	MGPLPRTVELFVDSLPSWLGIELCRYQNIWNTNLQRPLSLTGIMKDSCKPKPLGP	L	60			
Qy	1	RKGILYMANDLKLLRHHLOIPIHFKDFLSVMLKGSLSAMRELTAVNLEHPMLEKASRE	120				
Db	61	RKGILYMANDLKLLRHHLOIPIHFKDFLSVMLKGSLSAMRELTAVNLEHPMLEKASRE	120				
Qy	121	LWMRVMWSRNEDITEPOSTLAAAKGAMSSEQAQGLEKIAATPKVKNQLKEETEAACRGYA	180				
Db	121	LWMRVMWSRNEDITEPOSTLAAAKGAMSSEQAQGLEKIAATPKVKNQLKEETEAACRGYA	180				
Qy	181	FGLPITVAHVHDGQTHMLFGSDRMELLAHLLGEKNGMIPPAVNARL 226					
Db	181	FGLPITVAHVHDGQTHMLFGSDRMELLAHLLGEKNGMIPPAVNARL 226					

RESULT	2	Q9P1S4	PRELIMINARY;	PRT;	226 AA.		RESULT	4	Q9ZBY2	PRELIMINARY;	PRT;	305 AA.
ID	Q9P1S4;						ID	Q9ZBY2;				
AC	Q9P1S4;						AC	Q9ZBY2;				
DT	01-OCT-2000	(TREMBLrel. 15, Created)					DT	01-MAY-1999	(TREMBLrel. 10, Created)			
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)					DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)			
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)					DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)			
DE	HDCMD47P.						DE	HYPOTHETICAL 32.5 KDa PROTEIN.				
OS	Homo sapiens (Human).						GN	SCD8.17C.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						OS	Streptomyces coelicolor.				
OC	Mammalia; Actinobacteria; Actinomycetales; Streptomycetaceae; Streptomyces.						OC	Bacteria; Firmicutes; Actinobacteria; Streptomycetaceae; Streptomyces.				
OX	NCBI_TaxID=9606;						OC	Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.				
RN	[1]						OX	NCBI_TaxID=1902;				
RP	SEQUENCE FROM N.A.						RN	[1]				
RA	Zhao Z., Huang X., Li N., Zhu X., Cao X.;						RP	SEQUENCE FROM N.A.				
RT	"A novel gene from human dendritic cell."						RC	STRAIN=A3(2);				
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.						RA	Saunders D.C., Harris D.;				
DR	EMBL; AFO068287; AAF65506; -.						RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
SQ	SEQUENCE 226 AA;						RN	[2]				
Query Match	78.8%;	Score 178;	DB 4;	Length 226;			RP	SEQUENCE FROM N.A.				
Best Local Similarity	100.0%	Pred. No. 1	6e-172;				RC	STRAIN=A3(2);				
Matches	178;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	RC	REDENBACH M., KIESER H.M., DENPAITE D., EICHNER A., CULLUM J.,				
QY	1	MGLPLRPTVELFYDVLSPYSGNGFELLCRYQNYINWNINQLRPSLTGTGIMKDSGNKPGPLL 60					RC	MEDLINE-97000151; PubMed=8843436;				
Db	1	MGLPLRPTVELFYDVLSPYSGNGFELLCRYQNYINWNINQLRPSLTGTGIMKDSGNKPGPLL 60					RX	REDENBACH M., KIESER H.M., DENPAITE D., EICHNER A., CULLUM J.,				
QY	61	RKGLYMANDLKLLRHLQLPQTHPKDFLSVNLKGSLSAMRFLTAVNLHPEMLEKASRE 120					RA	KINASHI H., HOPWOOD D.A.;				
Db	61	RKGLYMANDLKLLRHLQLPQTHPKDFLSVNLKGSLSAMRFLTAVNLHPEMLEKASRE 120					RT	"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."				
QY	121	LWNRVWSRNEDITPEQSILAAEAERAGMSAEQAGLLEKIAATPKVKNQLKETTEAACRY 178					RT	RT				
Db	121	LWNRVWSRNEDITPEQSILAAEAKAGMSAEQAGLLEKIAATPKVKNQLKETTEAACRY 178					BL	BL				
QY	121	LWNRVWSRNEDITPEQSILAAEAERAGMSAEQAGLLEKIAATPKVKNQLKETTEAACRY 178					DR	MO. MICROBIOL 21:77-96 (1996).				
Db	121	LWNRVWSRNEDITPEQSILAAEAKAGMSAEQAGLLEKIAATPKVKNQLKETTEAACRY 178					DR	EMBL; AL034355; CA22222.1; -.				
Query Match	3.5%;	Score 8;	DB 4;	Length 283;			DR	INTERPRO; IPR000150; -.				
Best Local Similarity	100.0%	Pred. No. 7.1;					DR	PFAM; PF00592; DUF3.1.				
Matches	8;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	DR	KW. Hypothetical protein.				
SQ	SEQUENCE 283 AA;						SQ	SEQUENCE 305 AA;	32463 MW;	B8DCCB51C25E3B35 CRC64;		
RESULT	3	Q9U4L2	PRELIMINARY;	PRT;	283 AA.		Query Match	3.5%;	Score 8;	DB 2;	Length 305;	
ID	Q9U4L2						Best Local Similarity	100.0%	Pred. No. 7.5;	Mismatches 0;	Indels 0;	Gaps 0;
AC	Q9U4L2;						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
DT	01-MAY-2000	(TREMBLrel. 13, Created)					AC	094959;	PRELIMINARY;	PRT;	364 AA.	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)					AC	094959;	PRELIMINARY;	PRT;	364 AA.	
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)					AC	094959;	PRELIMINARY;	PRT;	364 AA.	
DE	PARANEOPLASTIC CANCER-TESTIS-BRAIN ANTIGEN (FRAGMENT).						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
GN	Homo sapiens (Human).						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
OC	NCBI_TaxID=9606;						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RN	[1]						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RP	SEQUENCE FROM N.A.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RA	Gultekin S.H., Voltz R., Rosenfeld M.R., Gerstner E., Eichen J., Posner J.B., Dalmat J.J.;						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RA	"Identification of a novel cancer testis brain antigen using serum antibodies from patients with testicular tumors and paraneoplastic limbic encephalomyelitis."						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RT	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RT	DR	EMBL; AF05626.1; -.					AC	094959;	PRELIMINARY;	PRT;	364 AA.	
FT	NON_TER	1					AC	094959;	PRELIMINARY;	PRT;	364 AA.	
SQ	SEQUENCE 283 AA;	32333 MW;	E2TB6BCDCD240A4 CRC64;				AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RESULT	4	Q9ZBY2	PRELIMINARY;	PRT;	305 AA.		AC	094959;	PRELIMINARY;	PRT;	364 AA.	
ID	Q9ZBY2;						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
AC	Q9ZBY2;						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
DT	01-MAY-1999	(TREMBLrel. 10, Created)					AC	094959;	PRELIMINARY;	PRT;	364 AA.	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)					AC	094959;	PRELIMINARY;	PRT;	364 AA.	
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)					AC	094959;	PRELIMINARY;	PRT;	364 AA.	
DE	HYPOTHETICAL 32.5 KDa PROTEIN.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
GN	SCD8.17C.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
OS	Streptomyces coelicolor.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
OC	Bacteria; Firmicutes; Actinobacteria; Streptomycetaceae; Streptomyces.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
OC	Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
OC	NCBI_TaxID=1902;						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RN	[1]						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RP	SEQUENCE FROM N.A.						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RA	Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RA	"Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."						AC	094959;	PRELIMINARY;	PRT;	364 AA.	
RA	DNA Res. 5:355-364 (1998).						AC	094959;	PRELIMINARY;	PRT;	364 AA.	

DR	EMBL; AB020690; BAA74906.1; -.	PRINTS; PR00049; WILMSTUMOUR.
SO	SEQUENCE 364 AA; 41509 MW;	DR PROSTE; PS00028; ZINC_FINGER_C2H2; 4.
	6E417AD96B3F0B93 CRC64;	SQ SEQUENCE 419 AA; 45925 MW; 606ADFEDA619EECD CRC64;
Query Match	3.5%; Score 8; DB 4; Length 364;	Query Match 3.5%; Score 8; DB 13; Length 419;
Best Local Similarity	100.0%; Pred. No. 8.8;	Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 0;	Indels 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	204 ELLAHLG 211	Qy 175 ACRYGAFG 182
Db	140 ELLAHLG 147	Db 91 ACRYGAFG 98
RESULT 6	PRELIMINARY: PRT: 392 AA.	RESULT 8
ID Q9IBFO	PRELIMINARY: PRT: 392 AA.	Q9W611 PRELIMINARY: PRT: 426 AA.
AC Q9IBFO;		ID Q9W611
DT 01-OCT-2000 (TREMBLrel. 15, Created)		AC Q9W611; CREATED
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)		DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE WILMS / TUMOR PROTEIN.		DE WT1.
GN OS		OS Cynops pyrrhogaster (Japanese common newt).
OS Anguilla japonica (Japanese eel).		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Cynops.
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillioidei; Anguillidae; Anguilla.		NCBI_TAXID=8330; [1]
OC NCBI_TAXID=937;		RN SEQUENCE FROM N.A.
RN [1]		RP TISSUE-TESTIS;
RP SEQUENCE FROM N.A.		RC NAKAYAMA Y., Yamamoto T., Matsuda Y., Abe S. I.;
RC TISSUE-KIDNEY;		RA Nakatsuru Y., Minami K., Yoshikawa A., Zhu J.J., Oda H., Masahito P.,
RA Nakatsuru Y., Minami K., Yoshikawa A., Zhu J.J., Oda H., Masahito P.,		RA "Cloning of cDNA for newt WT1 and the differential expression during spermatogenesis of the Japanese newt, Cynops pyrrhogaster,"
RA Okamoto N., Nakamura Y., Ishikawa T.; "Bel WT1 sequence and expression in spontaneous nephroblastomas in Japanese eel,"		RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RT Gene 245:245-251(2000);		RL EMBL: AB013888; BAA76399.1; -.
RT Gene 245:245-251(2000);		HSSP; P08046; 1AAY.
RL DR AB030741; BAA90558.1; -.		INTERPRO; IPR000822; -.
DR SEQUENCE 392 AA; 43892 MW; DAE1A84828F4 3DF6 CRC64;		INTERPRO; IPR000976; -.
DR SEQUENCE 392 AA; 43892 MW; DAE1A84828F4 3DF6 CRC64;		PFAM; PF00096; zf-C2H2; 4.
Query Match 3.5%; Score 8; DB 13; Length 392;		PRINTS; PR00049; ZINC_FINGER_C2H2; 4.
Best Local Similarity 100.0%; Pred. No. 9.3;		DR PROSTE; PS00028; ZINC_FINGER_C2H2; 4.
Matches 8; Conservative 0; Mismatches 0;		KW Zinc-finger; Metal-binding; DNA-binding.
Indels 0;		SQ SEQUENCE 426 AA; 47590 MW; 46A0B158A9F79C6C CRC64;
Gaps 0;		
Qy 175 ACRYGAFG 182		Query Match 3.5%; Score 8; DB 13; Length 426;
Db 91 ACRYGAFG 99		Best Local Similarity 100.0%; Pred. No. 10.0%; Mismatches 0; Indels 0; Gaps 0;
RESULT 7	PRELIMINARY: PRT: 419 AA.	Qy 175 ACRYGAFG 182
ID Q9PUT7	PRELIMINARY: PRT: 419 AA.	Db 90 ACRYGAFG 97
AC Q9PUT7;		RESULT 9
DT 01-MAY-2000 (TREMBLrel. 13, Created)		085409 PRELIMINARY; PRT: 83 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		ID 085409
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)		AC 085409; CREATED
DE WILMS / TUMOR SUPPRESSOR.		DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
OS Brachydanio rerio (Zebrafish) (Zebra danio).		DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysii; Cypriniformes; Cyprinidae; Rasborinae; Danio.		DT MAJOR_OUTER_MEMBRANE_LIPOPROTEIN_I (FRAGMENT).
OC NCBI_TAXID=7935;		DE OPRI.
OX RN SEQUENCE FROM N.A.		OS Pseudomonas mendocina.
RA Smith S.I., Down M., Boyd A.W.; "Isolation and characterization of a cDNA encoding zebrafish (Danio rerio) WT-1."		OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.		NCBI_TAXID=300; [1]
RL STRAIN=LMG 1223;		RN SEQUENCE FROM N.A.
DR HSSP; AF144550; AA00123.1; -.		RP MEDLINE#8931294; PubMed=2473376;
DR INTERPRO; IPR000822; -.		RX Cornelis P., Boula A., Belarbi A., Guyonvarch A., Kammerer B.,
DR INTERPRO; IPR000976; -.		RA Hannaert V., Hubert J.C.; Cloning and analysis of the gene for the major outer membrane
DR PFAM; PF00096; zf-C2H2; 4.		RT PFAM; PF02165; WT1; 3.
DR PFAM; PF02165; WT1; 3.		

RT lipoprotein from *Pseudomonas aeruginosa*.";
 RL Mol. Microbiol. 3:421-428(1989).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 12229;
 RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,
 Cornelis P.;
 "Sequence diversity of the oprI gene coding for the major outer
 membrane lipoprotein I among rRNA group I pseudomonads.",
 DR Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 EMBL; AF065948; AAD03503.1; -.

KW Lipoprotein.
 FT NON_TER 83 83 AA; 8843 MW; EF0F54D80801DBA1 CRC64;
 SQ SEQUENCE 83 AA; 8843 MW; EF0F54D80801DBA1 CRC64;

Query Match 3.1%; Score 7; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 113 MLEKASR 119
 Db 76 MLEKASR 82

RESULT 10
 O85410 PRELIMINARY; PRT; 83 AA.
 ID O85410; AC 085410;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE MAJOR OUTER MEMBRANE LIPOPROTEIN I (FRAGMENT).
 GN OPRI.
 OS *Pseudomonas oleovorans*.
 OC Bacteria; Proteobacteria; gamma subdivision; *Pseudomonadaceae*;
 OC *Pseudomonas*.
 OX NCBI_TAXID=301;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 2229;
 RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,
 Hannaert V., Hubert J.C.;
 "Cloning and analysis of the gene for the major outer membrane
 lipoprotein from *Pseudomonas aeruginosa*.",
 RL Mol. Microbiol. 3:421-428(1989).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 2229;
 RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,
 Cornelis P.;
 "Sequence diversity of the oprI gene coding for the major outer
 membrane lipoprotein I among rRNA group I pseudomonads.",
 DR Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 EMBL; AF065949; AAD03504.1; -.

FT NON_TER 83 83 AA; 8801 MW; EF0123A10676A2A1 CRC64;
 SQ SEQUENCE 83 AA; 8801 MW; EF0123A10676A2A1 CRC64;

Query Match 3.1%; Score 7; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 113 MLEKASR 119
 Db 76 MLEKASR 82

RESULT 11
 O85411 PRELIMINARY; PRT; 83 AA.
 ID O85411; AC 085411;

Fri Apr 20 10:52:41 2001

us-09-441-723-1.rspt

Page 6

Db 76 MLEKASR 82

Search completed: April 19, 2001, 13:00:36
Job time: 119 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2001, 12:58:12 ; search time 4.15 Seconds
(without alignments)
137.860 Million cell updates/sec

Title: US-09-441-723-1
Perfect score: 226
Sequence: 1 MGPLRPTVBLFYDVLSPYSW.....AHLLGKWMGPIPPAVNARL 226

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 12259 seqs, 2531507 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/podata/ca/1/paa/pctc/_NEW_COMB.pep:
2: /cgn2_6/podata/ca/1/paa/us06__NEW_COMB.pep:
3: /cgn2_6/podata/ca/1/paa/us07__NEW_COMB.pep:
4: /cgn2_6/podata/ca/1/paa/us08__NEW_COMB.pep:
5: /cgn2_6/podata/ca/1/paa/us60__NEW_COMB.pep:
6: /cgn2_6/podata/ca/1/paa/us60__NEW_COMB.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	7	3.1	261	5	US-09-739-449-11148	Sequence 11148, A
2	7	3.1	688	6	US-60-248-505-865	Sequence 865, APP
3	6	2.7	62	5	US-09-739-449-10531	Sequence 10531, A
4	6	2.7	161	5	US-09-739-449-12044	Sequence 12044, A
5	6	2.7	207	5	US-09-739-449-9529	Sequence 9529, AP
6	6	2.7	215	5	US-09-739-449-9343	Sequence 9343, AP
7	6	2.7	235	5	US-09-739-449-9873	Sequence 9873, AP
8	6	2.7	235	5	US-09-739-449-10784	Sequence 10784, A
9	6	2.7	245	5	US-09-739-449-10257	Sequence 10257, A
10	6	2.7	258	5	US-09-739-449-10586	Sequence 10586, A
11	6	2.7	305	5	US-09-739-449-9486	Sequence 9486, AP
12	6	2.7	315	5	US-09-739-449-11093	Sequence 11093, A
13	6	2.7	325	5	US-09-739-449-1418	Sequence 1418, A
14	6	2.7	327	5	US-09-739-449-13257	Sequence 13257, A
15	6	2.7	329	5	US-09-739-449-12591	Sequence 12591, A
16	6	2.7	337	5	US-09-739-449-11560	Sequence 11560, A
17	6	2.7	338	5	US-09-739-449-12951	Sequence 12951, A
18	6	2.7	447	5	US-09-739-449-11196	Sequence 11196, A
19	6	2.7	456	5	US-09-739-449-13245	Sequence 13245, A
20	6	2.7	474	5	US-09-739-449-11298	Sequence 11298, A
21	6	2.7	496	6	US-60-248-505-1273	Sequence 1273, AP
22	6	2.7	570	6	US-60-248-505-980	Sequence 980, APP
23	6	2.7	730	6	US-60-248-505-921	Sequence 921, APP
24	6	2.7	926	5	US-09-421-124-187	Sequence 187, APP
25	6	2.7	926	5	US-09-421-124-187	Sequence 187, APP
26	6	2.7	1116	5	US-09-739-449-11359	Sequence 11359, A
27	6	2.7	2882	6	US-60-248-505-1095	Sequence 1095, AP

ALIGNMENTS

RESULT 1
US-09-739-449-11148
; Sequence 11148, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; INVENTOR: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10154901C
; CURRENT APPLICATION NUMBER: US/09-739-449-11782
; CURRENT FILING DATE: 2000-12-19
; PRIORITY APPLICATION NUMBER: US 09-514,000
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO: 11148
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-11148

Query Match 3.18; Score 7; DB 5; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 AAAEKAG 146
Db 50 AAAEKAG 56

RESULT 2
US-60-248-505-865
; Sequence 865, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 865
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Human
US-60-248-505-865

Query Match 3.18; Score 7; DB 6; Length 688

Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 9529
LENGTH: 207

RESULT 3
US-09-739-449-10531
Sequence 10531, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 10531
LENGTH: 62

TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-10531

Query Match 2.7%; Score 6; DB 5;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 167 QLKETT 172
Db 5 QLKETT 10

RESULT 4
US-09-739-449-12044
Sequence 12044, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 12044
LENGTH: 161

TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-12044

Query Match 2.7%; Score 6; DB 5;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 104 TAVNLE 109
Db 153 TAVNLE 158

RESULT 5
US-09-739-449-9529
Sequence 9529, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9529
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
; US-09-739-449-9529

Query Match 2.7%; Score 6; DB 5;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 138 ILAAAE 143
Db 15 ILAAAE 20

RESULT 6
US-09-739-449-9343
Sequence 9343, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 9343
LENGTH: 215

TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9343

Query Match 2.7%; Score 6; DB 5;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 139 LAAEAK 144
Db 159 LAAEAK 164

RESULT 7
US-09-739-449-9873
Sequence 9873, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 9873
LENGTH: 235

TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9873

Query Match 2.7%; Score 6; DB 5;
Best Local Similarity 100.0%; Pred. No. 23;

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; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIORITY APPLICATION NUMBER: US 09/514,000
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO: 10586
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-10586

RESULT 8
US-09-739-449-10784
GENERAL INFORMATION:
SEQUENCE 10784, Application US/09739449
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIORITY APPLICATION NUMBER: US 09/514,000
PRIORITY FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO: 10784
LENGTH: 235
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-10784

Query Match 2.7%; Score 6; DB 5; Length 258;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 2.7%; Score 6; DB 5; Length 258;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; SEQUENCE 9486, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIORITY APPLICATION NUMBER: US 09/514,000
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO: 9486
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9486

RESULT 11
US-09-739-449-9486
; SEQUENCE 9486, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIORITY APPLICATION NUMBER: US 09/514,000
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO: 9486
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9486

Query Match 2.7%; Score 6; DB 5; Length 305;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 2.7%; Score 6; DB 5; Length 305;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; SEQUENCE 1.1093, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIORITY APPLICATION NUMBER: US 09/514,000
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO: 11093
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-11093

RESULT 12
US-09-739-449-11093
; SEQUENCE 1.1093, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIORITY APPLICATION NUMBER: US 09/514,000
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO: 11093
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-11093

Query Match 2.7%; Score 6; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 2.7%; Score 6; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; SEQUENCE 10586, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIORITY APPLICATION NUMBER: US 09/514,000
; PRIORITY FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO: 10586
; LENGTH: 315;
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-10586

Query Match 2.7%; Score 6; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 179 GAFGLP 184 ; CURRENT FILING DATE: 2000-12-19
 Db 250 GAFGLP 255 ; PRIOR APPLICATION NUMBER: US 09/514,000

RESULT 13 ;
 ; Sequence 12418, Application US/09739449

; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences' and Uses Thereof
 ; FILE REFERENCE: 8-10(15490)C
 ; CURRENT APPLICATION NUMBER: US/09/739,449
 ; CURRENT FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIORITY FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO: 12418
 ; LENGTH: 325
 ; TYPE: PRT
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-739-449-12418

Query Match 2.7%; Score 6; DB 5; Length 325;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0;
 Qy 140 AAAEKA 145 Indels 0; Gaps 0;
 Db 81 AAAEKA 86

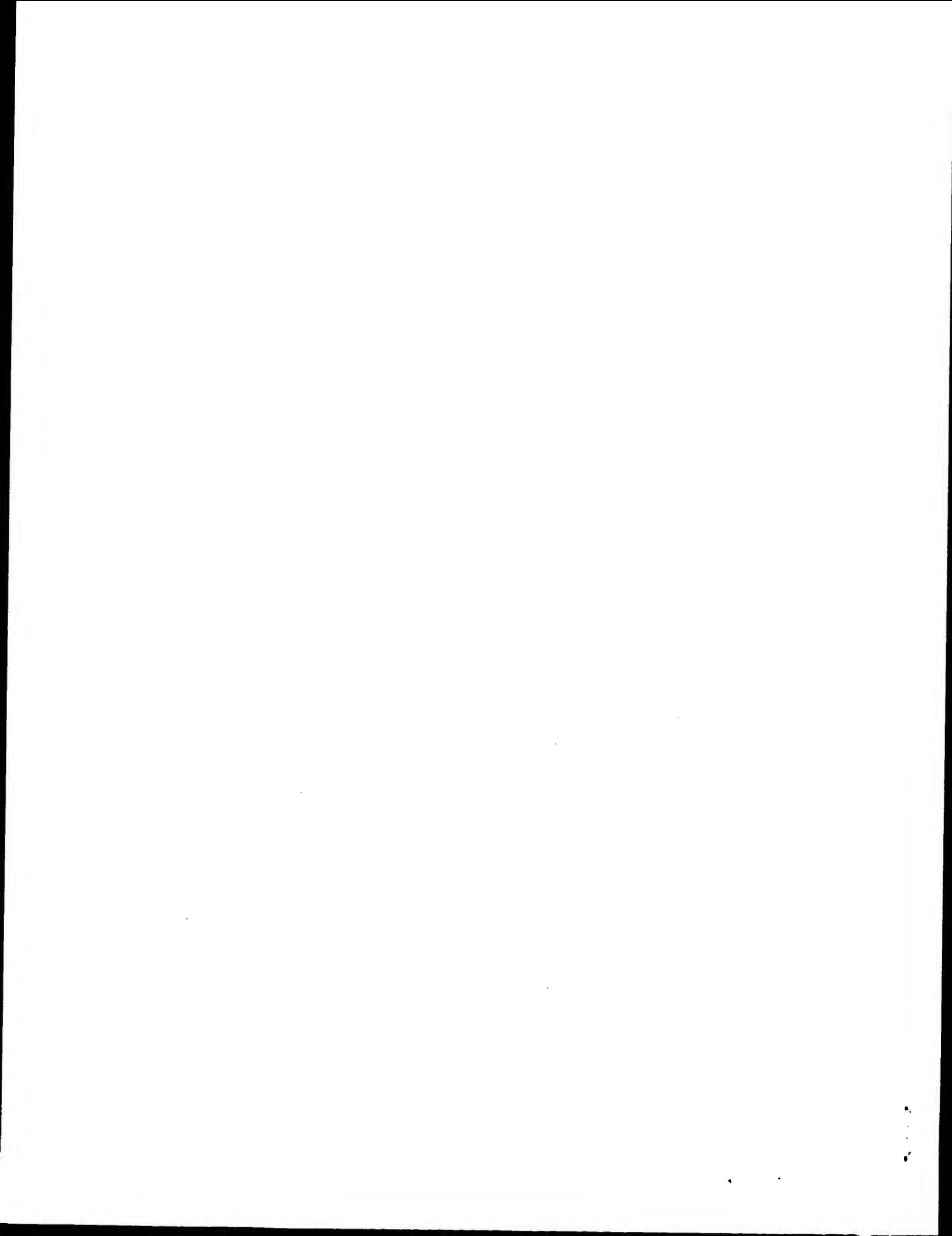
RESULT 14 ;
 ; Sequence 13257, Application US/09739449

; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)C
 ; CURRENT APPLICATION NUMBER: US/09/739,449
 ; CURRENT FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIORITY FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO: 13257
 ; LENGTH: 327
 ; TYPE: PRT
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-739-449-13257

Query Match 2.7%; Score 6; DB 5; Length 327;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0;
 Qy 153 QGLEEK 158 Indels 0; Gaps 0;
 Db 59 QGLEEK 64

RESULT 15 ;
 ; Sequence 12591, Application US/09739449

; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)C
 ; CURRENT APPLICATION NUMBER: US/09/739,449



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2001, 12:58:02 ; Search time 44.47 Seconds

(without alignments)
 817.475 Million cell updates/secTitle: US-09-441-723-1
 Perfect score: 226
 Sequence: 1 MGDLPRTYVELFYDVLSPYSW.....AHLGEKWMGPIPPAVNARL 226

Scoring table:

OLIGO Gapext 60.0 , Gapext 60.0

Searched: 1009251 seqs, 160854530 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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23:

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 12 8 3.5 195 15 US-09-189-527-7
 13 8 3.5 814 6 US-08-233-642A-40
 14 7 3.1 46 23 US-60-186-652-1013
 15 7 3.1 55 8 US-08-124-550A-493
 16 7 3.1 55 8 US-08-169-260-493
 17 7 3.1 55 8 US-08-469-260A-493
 18 7 3.1 55 8 US-08-468-749-493
 19 7 3.1 55 8 US-08-468-445A-493
 20 7 3.1 55 8 US-08-446-493
 21 7 3.1 55 8 US-08-448-446-493
 22 7 3.1 63 9 US-08-572-447B-9
 23 7 3.1 63 16 US-09-267-747-9
 24 7 3.1 75 18 US-09-417-507-24513
 25 7 3.1 78 16 US-60-196-712-3205
 26 7 3.1 91 23 US-60-196-711-2061
 27 7 3.1 93 23 US-60-196-711-2062
 28 7 3.1 104 16 US-09-252-991A-26172
 29 7 3.1 130 1 PCP-US00-05918-854
 30 7 3.1 132 16 US-09-270-767-36291
 31 7 3.1 132 16 US-09-270-767-51508
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 33 7 3.1 133 4 US-08-047-167-3
 34 7 3.1 133 12 US-08-80-741-19
 35 7 3.1 136 16 US-09-270-767-37986
 36 7 3.1 141 1 PCT-US99-22853B-972
 37 7 3.1 142 1 PCT-US99-22853B-971
 38 7 3.1 161 23 US-00-207-583-340
 39 7 3.1 204 10 US-08-691-814-10
 40 7 3.1 204 10 US-08-691-814A-10
 41 7 3.1 204 16 US-09-250-609-4
 42 7 3.1 204 16 US-09-250-609-9
 43 7 3.1 204 16 US-09-250-609-9
 44 7 3.1 204 16 US-09-250-609-9
 45 7 3.1 204 16 US-09-250-611-4

ALIGNMENTS

RESULT¹

US-09-441-723-1

Sequence 1, Application US/09441723

GENERAL INFORMATION:

APPLICANT: Shah, Purvi

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Corley, Neill C.

TITLE OF INVENTION: NEW GLUTATHIONE-S-TRANSFERASE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/441,723

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/978,174

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0430 US

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	226	100.0	226	18	US-09-441-723-1
2	150	66.4	150	23	US-60-147-499-4666
3	97	42.9	97	1	PCT-US00-06824-176
4	92	40.7	120	23	US-60-245-201-153
5	92	40.7	120	23	US-60-245-201-226
6	16	7.1	226	18	US-69-441-723-3
7	12	5.3	97	1	PCT-US00-06824-175
8	8	3.5	91	16	US-09-252-991A-23967
9	8	3.5	173	18	US-09-489-039A-7934
10	8	3.5	179	1	PCT-US00-05918-529

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 226 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BLADUT04
 CLONE: 1554593
 US-09-441-723-1

Query Match 100.0% Score 226; DB 18; Length 226;
 Best Local Similarity 100.0%; Pred. No. 9; Be-224; Length 226;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPLPRTVLEFYDVLSPYSWLGFEILCRQNIWNINLQLRPSLITGIMKDSGNKPGLP 60
 Db 1 MGPLPRTVLEFYDVLSPYSWLGFEILCRQNIWNINLQLRPSLITGIMKDSGNKPGLP 60

Qy 61 RKGLYMANDKLRRHHLQIPIHPKDFLSVMLEKGSLSAMRFILTAVNLEHPEMLEKASRE 120
 Db 61 RKGLYMANDKLRRHHLQIPIHPKDFLSVMLEKGSLSAMRFILTAVNLEHPEMLEKASRE 120

Qy 121 LWMRVWSRNEDITEPOSILAAEAKGMSAEQAGLLEKIAATPKVKQNOLKETTEAACRYGA 180
 Db 121 LWMRVWSRNEDITEPOSILAAEAKGMSAEQAGLLEKIAATPKVKQNOLKETTEAACRYGA 180

Qy 181 FGLPITVAVGQTHMLFGSDRMELLAHLGEKWMGPPIPPAVNRL 226
 Db 181 FGLPITVAVGQTHMLFGSDRMELLAHLGEKWMGPPIPPAVNRL 226

RESULT 2 US-60-147-499-4666
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET_05APR2
 ; CURRENT APPLICATION NUMBER: US/60/147,499
 ; CURRENT FILING DATE: 1999-08-05
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pmm
 ; SEQ ID NO 4666
 ; LENGTH: 150
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-147-499-4666

Query Match 66.4% Score 150; DB 23; Length 150;
 Best Local Similarity 100.0%; Pred. No. 8.8e-146; Length 150;
 Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPLPRTVLEFYDVLSPYSWLGFEILCRQNIWNINLQLRPSLITGIMKDSGNKPGLP 60
 Db 1 MGPLPRTVLEFYDVLSPYSWLGFEILCRQNIWNINLQLRPSLITGIMKDSGNKPGLP 60

Qy 61 RKGLYMANDKLRRHHLQIPIHPKDFLSVMLEKGSLSAMRFILTAVNLEHPEMLEKASRE 120
 Db 61 RKGLYMANDKLRRHHLQIPIHPKDFLSVMLEKGSLSAMRFILTAVNLEHPEMLEKASRE 120

RESULT 2 US-60-147-499-4666
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: 47 Human Secreted Proteins
 ; FILE REFERENCE: PS511PCT
 ; CURRENT APPLICATION NUMBER: PCT/US00/06824
 ; CURRENT FILING DATE: 2000-03-16
 ; EARLIER APPLICATION NUMBER: 60/125,359
 ; EARLIER FILING DATE: 1999-03-19
 ; EARLIER APPLICATION NUMBER: 60/168,664
 ; EARLIER FILING DATE: 1999-12-03
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 176

Query Match 42.9% Score 97; DB 1; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91; Length 97;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 EDITEPOSTLAAEAKGMSAEQAGLLEKIAATPKVKQNOLKETTEAACRYGAFLGPLTVAH 189
 Db 1 EDITEPOSTLAAEAKGMSAEQAGLLEKIAATPKVKQNOLKETTEAACRYGAFLGPLTVAH 60

Qy 190 VDGQTHMLFGSDRMELLAHLGEKWMGPPIPPAVNRL 226
 Db 61 VDGQTHMLFGSDRMELLAHLGEKWMGPPIPPAVNRL 97

RESULT 4 US-60-245-201-153
 ; Sequence 153, Application US/60245201
 ; GENERAL INFORMATION:
 ; APPLICANT: Beasley, Ellen
 ; TITLE OF INVENTION: ISOLATED HUMAN PHASE II DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREFOR
 ; FILE REFERENCE: CL000879
 ; CURRENT APPLICATION NUMBER: US/60/245,201
 ; CURRENT FILING DATE: 2000-11-03
 ; NUMBER OF SEQ ID NOS: 381
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 153
 ; LENGTH: 120
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-60-245-201-153

Query Match 40.7% Score 92; DB 23; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.9e-86; Length 120;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 PQSILAAEAKGMSAEQAGLLEKIAATPKVKQNOLKETTEAACRYGAFLGPLTVAHVDGQT 194
 Db 29 PQSILAAEAKGMSAEQAGLLEKIAATPKVKQNOLKETTEAACRYGAFLGPLTVAHVDGQT 88

Qy 195 HMLFGSDRMELLAHLGEKWMGPPIPPAVNRL 226
 Db 89 HMLFGSDRMELLAHLGEKWMGPPIPPAVNRL 120

RESULT 5 US 60-245-201-226
 ; Sequence 226, Application US/60245201
 ; GENERAL INFORMATION:

APPLICANT: Beasley, Ellen
 TITLE OF INVENTION: ISOLATED HUMAN PHASE II, NUCLEIC ACID MOLECULES ENCODING DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
 FILE REFERENCE: CL000879
 CURRENT APPLICATION NUMBER: US/60/245,201
 NUMBER OF SEQ ID NOS: 381
 CURRENT FILING DATE: 2000-11-03
 SOFTWARE: FastSEQ For Windows Version 4.0
 SEQ ID NO: 226
 LENGTH: 120
 TYPE: PRT
 ORGANISM: Human
 US-60-245-201-226

RESULT 6
 US-09-441-723-3
 Sequence 3, Application US/09441723
 GENERAL INFORMATION:
 APPLICANT: Shah, Purvi
 APPLICANT: Hilman, Jennifer L.
 APPLICANT: Lal, Preeti
 APPLICANT: Corley, Neill C.
 TITLE OF INVENTION: NEW GLUTATHIONE-S-TRANSFERASE
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/441,723
 FILING DATE:
 CLASSIFICATION:
 APPLICATION NUMBER: 08/978,174
 PRIORITY APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0430 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 226 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:

LIBRARY: GenBank
 CLONE: ?
 US-09-441-723-3

Query Match 40.7%; Score 92; DB 23; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.9e-86;
 Matches 92; Conservative 0; Indels 0; Gaps 0;

Qy 135 POSTLAAAEATAGMSAEQAQGLILEKATPKVNQLKETTEAACRYGAAGLPLTVAHVDQQT 194
 Db 29 POSTLAAAEATAGMSAEQAQGLILEKATPKVNQLKETTEAACRYGAAGLPLTVAHVDQQT 88

Qy 195 HMLFGSDRMELLAHLIGEKNMGPIPPAVNRL 226
 Db 89 HMLFGSDRMELLAHLIGEKNMGPIPPAVNRL 120

RESULT 7
 PCT-US00-06824-175
 Sequence 175, Application PC/TUS0006824
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 TITLE OF INVENTION: Human Secreted Proteins
 FILE REFERENCE: PSS11.PCT
 CURRENT APPLICATION NUMBER: PCT/US00/06824
 CURRENT FILING DATE: 2000-03-16
 EARLIER APPLICATION NUMBER: 60/125,359
 EARLIER FILING DATE: 1999-03-19
 EARLIER APPLICATION NUMBER: 60/168,664
 EARLIER FILING DATE: 1999-12-03
 NUMBER OF SEQ ID NOS: 180
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 175
 LENGTH: 97
 TYPE: PRT
 ORGANISM: Homo sapiens
 PCT-US00-06824-175

Query Match 5.3%; Score 12; DB 1; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.0004;
 Matches 12; Conservative 0; Indels 0; Gaps 0;

Qy 196 MLFGSDRMELIA 207
 Db 67 MLFGSDRMELIA 78

RESULT 8
 US-09-252-991A-23967
 Sequence 23967, Application US/09252991A
 GENERAL INFORMATION:
 APPLICANT: Rubenfield et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 23967
 LENGTH: 91
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-23967

Query Match 3.5%; Score 8; DB 16; Length 91;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 8; Conservative 0; Indels 0; Gaps 0;

Qy 149 AEQAQGLL 156
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Db 79 AEQAQGLL 86

RESULT 9
US-09-489-039A-7934
; Sequence 7934, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004/001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7934
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7934

Query Match
Best Local Similarity 3.5%; Score 8; DB 15; Length 195;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: homo sapiens
US-09-189-527-7

Query Match
Best Local Similarity 3.5%; Score 8; DB 15; Length 195;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: homo sapiens
US-09-189-527-7

RESULT 12
US-09-189-527-7
; Sequence 7, Application US/09189527A
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Joseph O. Dalmau
; APPLICANT: Myrna R. Rosenfeld
; TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma
; FILE REFERENCE: SUK98-01
; CURRENT APPLICATION NUMBER: US/09/189,527A
; CURRENT FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 195
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-189-527-7

Query Match
Best Local Similarity 3.5%; Score 8; DB 15; Length 195;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: homo sapiens
US-09-189-527-7

RESULT 10
PCT-US00-05918-529
; Sequence 529, Application PC/TUS00005918
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Human Lung Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: P1010/PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05918
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 529
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-05918-529

Query Match
Best Local Similarity 3.5%; Score 8; DB 1; Length 179;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens
PCT-US00-05918-529

RESULT 11
US-09-189-527-7
; Sequence 7, Application US/09189527
; GENERAL INFORMATION:
; APPLICANT: Jerome B. Posner
; APPLICANT: Joseph O. Dalmau
; APPLICANT: Myrna R. Rosenfeld
; TITLE OF INVENTION: Ma Family Polypeptides and Anti-Ma Antibodies
; FILE REFERENCE: SUK98-01
; CURRENT APPLICATION NUMBER: US/09/189,527
; CURRENT FILING DATE: 1998-11-10
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/233,642A
 FILING DATE: 26-APR-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: King, Joshua
 REGISTRATION NUMBER: 35,570
 REFERENCE/DOCKET NUMBER: 920043.403C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 TELEX: 3723836 SEEDANBERRY
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 814 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-233-642A-40

Query Match 3.5%; Score 8; DB 6; Length 814;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 NOLKETTE 173
 Db 60 NOLKETTE 67

RESULT 14
 US-60-186-662-1013
 GENERAL INFORMATION:
 APPLICANT: Bonazzi, Vivien
 TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
 NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
 TITLE OF INVENTION: AND USES THEREOF
 FILE REFERENCE: CL000314
 CURRENT APPLICATION NUMBER: US/60/186,662
 CURRENT FILING DATE: 2000-03-03
 NUMBER OF SEQ ID NOS: 1080
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1013
 LENGTH: 46
 TYPE: PRT
 ORGANISM: HUMAN
 US-60-186-662-1013

Query Match 3.1%; Score 7; DB 23; Length 46;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 PPGLLPR 61
 Db 40 PPGLLPR 46

RESULT 15
 US-08-424-550A-493
 Sequence 493, Application US/08424550A
 GENERAL INFORMATION:
 APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER
 APPLICANT: SURBESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT MUERHOF
 APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BULJK
 APPLICANT: ISA K. MUSHAHWAR
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08/424,550A
 APPLICATION NUMBER: US-08/424,550A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMISKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 493:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 55 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-424-550A-493

Query Match 3.1%; Score 7; DB 8;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 GSLSAMR 101
 Db 42 GSLSAMR 48

Search completed: April 19, 2001, 13:00:00
 Job time: 118 sec

